GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 05:21:14 ; Search time 294 Seconds
(without alignments)
644.326 Million cell updates/sec

Title: US-10-076-674A-1
Perfect score: 32
Sequence: 1 tcgtcgttttgtcgttttgtcgttttgtcgtt 32

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4333176

Minimum DB seq length: 0
Maximum DB seq length: 64

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	32	4	AAF99300	Aaf99300 Immunosti
2	32	100.0	32	6	ABS77945	Abs77945 Angiogene
3	32	100.0	32	6	ABL39305	Abl39305 Immunosti
4	32	100.0	32	9	ACD99725	Acd99725 Immunosti
5	32	100.0	32	9	ADB36802	Adb36802 Immunosti
6	32	100.0	32	10	ADD89955	Add89955 CpG oligo
7	32	100.0	32	12	ADJ56900	Adj56900 CpG oligo
8	26	81.2	27	9	ACD91394	Acd91394 Adjuvant-
9	26	81.2	29	4	AAF99178	Aaf99178 Immunosti
10	26	81.2	29	6	ABS77821	Abs77821 Angiogene
11	26	81.2	29	6	ABL38761	Abl38761 Immunosti
12	26	81.2	29	9	ACD99609	Acd99609 Immunosti
13	26	81.2	29	9	ADB36680	Adb36680 Immunosti
14	25	78.1	48	12	ADE39672	Ade39672 Oligonucl
15	25	78.1	52	2	AAV83725	Aav83725 Plasmid p
16	24	75.0	24	2	AAV60953	Aav60953 Unmethyla
17	24	75.0	24	2	AAV47689	Aav47689 Unmethyla
18	24	75.0	24	2	AAV27664	Aav27664 Immunosti
19	24	75.0	24	2	AAZ41936	Aaz41936 IL-12 sec
20	24	75.0	24	2	AAV83715	Aav83715 Synthetic
21	24	75.0	24	2	AAV74252	Aav74252 CpG-N mot
22	24	75.0	24	3	AAZ61001	Aaz61001 Nucleotid
23	24	75.0	24	3	AAZ48012	Aaz48012 Immune re
24	24	75.0	24	3	AAZ47876	Aaz47876 Immunosti
25	24	75.0	24	3	AAA39265	Aaa39265 CpG immun
26	24	75.0	24	3	AAZ47671	Aaz47671 Parasitic
27	24	75.0	24	3	AAA63588	Aaa63588 Immune st
28	24	75.0	24	3	AAA63586	Aaa63586 Immune st
29	24	75.0	24	3	AAA63598	Aaa63598 Immune st
30	24	75.0	24	3	AAC60280	Aac60280 Immunosti
31	24	75.0	24	3	AAA93700	Aaa93700 Unmethyla
32	24	75.0	24	4	AAC87240	Aac87240 CpG oligo
33	24	75.0	24	4	AAC87232	Aac87232 Immunosti
34	24	75.0	24	4	AAC87231	Aac87231 5'-amidat
35	24	75.0	24	4	AAC87233	Aac87233 Immunosti
36	24	75.0	24	4	AAC87227	Aac87227 Methylate
37	24	75.0	24	4	AAC87234	Aac87234 Digoxigen
38	24	75.0	24	4	AAC87237	Aac87237 5'-amidat
39	24	75.0	24	4	AAC87222	Aac87222 Immunosti
40	24	75.0	24	4	AAH50616	Aah50616 Cytokine
41	24	75.0	24	4	AAF98866	Aaf98866 CpG immun
42	24	75.0	24	4	AAF98732	Aaf98732 Human IFN
43	24	75.0	24	4	AAF98830	Aaf98830 CpG immun
44	24	75.0	24	4	AAF85631	Aaf85631 Vaccine a
45	24	75.0	24	4	AAF59508	Aaf59508 Immunosti

ALIGNMENTS

RESULT 1
AAF99300
ID AAF99300 standard; DNA; 32 BP.
XX
AC AAF99300;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #416.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 46; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory

CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 32 BP; 0 A; 5 C; 8 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 2
ABS77945
ID ABS77945 standard; DNA; 32 BP.
XX
AC ABS77945;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #429.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 27; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 32 BP; 0 A; 5 C; 8 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 3
ABL39305
ID ABL39305 standard; DNA; 32 BP.
XX
AC ABL39305;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 734.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .32
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 283; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 32 BP; 0 A; 5 C; 8 G; 19 T; 0 U; 0 Other;

```
  Query Match           100.0%;  Score 32;  DB 6;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
              ||||||||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32


RESULT 4
ACD99725
ID   ACD99725 standard; DNA; 32 BP.
XX
AC   ACD99725;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #411.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 19; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 32 BP; 0 A; 5 C; 8 G; 19 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 32;  DB 9;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
              ||||||||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32


RESULT 5
ADB36802
ID   ADB36802 standard; DNA; 32 BP.
XX
AC   ADB36802;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #416.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 11; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 32 BP; 0 A; 5 C; 8 G; 19 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 32;  DB 9;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-07;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
              ||||||||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32


RESULT 6
ADD89955
ID   ADD89955 standard; DNA; 32 BP.
XX
AC   ADD89955;
XX
DT   29-JAN-2004  (first entry)
XX
DE   CpG oligonucleotide used in immunostimulant complex.
XX
KW   Immunostimulant; vaccine; CpG; adjuvant; ss.
XX
OS   Synthetic.
XX
PN   WO2003068169-A2.
XX
PD   21-AUG-2003.
XX
PF   14-FEB-2003; 2003WO-US004711.
XX
PR   14-FEB-2002; 2002US-00076674.
PR   31-JAN-2003; 2003US-00076674.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
```

XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 10; SEQ ID NO 1; 159pp; English.
XX
CC The present sequence is that of an CpG oligonucleotide, denoted CpG1,
CC that is used in immunostimulatory complexes specifically adapted to act
CC as adjuvant and as peptide immunogen stabiliser. The complexes comprise a
CC CpG oligonucleotide and a biologically active peptide immunogen. The
CC complex is particulate and can efficiently present peptide immunogens to
CC the cells of the immune system to produce an immune response. The
CC complexes may be prepared with various ratios of peptides to CpG
CC oligonucleotides to provide different physical properties, such as the
CC size of the microparticle. CpG1 possesses a CpG motif sequestered within
CC a sequence of 8 nucleotide bases and may provide stronger adjuvantation
CC in vivo and improved stability by binding cationic peptides with higher
CC affinities than shorter oligonucleotides. Peptide immunogens used in
CC claimed immunostimulatory complexes are: LHRH peptides useful in a
CC vaccine for prostate cancer immunotherapy; CD4 peptides useful in an anti
CC -CD4 immunotherapeutic vaccine for the treatment of HIV infection; IgE
CC peptides useful in an allergy vaccine; and foot-and-mouth-disease
CC peptides useful in a vaccine.
XX
SQ Sequence 32 BP; 0 A; 5 C; 8 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 7
ADJ56900
ID ADJ56900 standard; DNA; 32 BP.
XX
AC ADJ56900;
XX
DT 06-MAY-2004 (first entry)
XX
DE CpG oligonucleotide, CpG1.
XX
KW Immunostimulatory complex; adjuvant; peptide immunogen stabiliser;
KW water-in-oil emulsion; suspension; vaccine; prostate cancer;
KW hormone ablation; allergy; HIV infection; foot-and-mouth disease;
KW therapy; ss.
XX
OS Synthetic.
XX
PN US2004009897-A1.
XX
PD 15-JAN-2004.
XX
PF 21-MAY-2003; 2003US-00355161.
XX
PR 14-FEB-2002; 2002US-00076674.
XX
PA (SOKO/) SOKOLL K K.
XX
PI Sokoll KK;
XX
DR WPI; 2004-212745/20.
XX
PT Stabilized immunostimulatory complex useful for treating allergy, HIV
PT infection or prostate cancer, comprising cationic peptide immunogen and
PT anionic CpG oligonucleotide.
XX
PS Claim 10; SEQ ID NO 1; 63pp; English.
XX
CC The invention relates to an immunostimulatory complex specifically
CC adapted to act as adjuvant and as a peptide immunogen stabiliser. The
CC invention is useful for preparing a water-in-oil emulsion, suspension and
CC vaccine. It is also useful for treating prostate cancer, hormone
CC ablation, allergy, HIV infection, foot-and-mouth disease, etc. The
CC present sequence is an oligonucleotide used in the invention.
XX
SQ Sequence 32 BP; 0 A; 5 C; 8 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 32; DB 12; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 8
ACD91394
ID ACD91394 standard; DNA; 27 BP.
XX
AC ACD91394;
XX
DT 22-SEP-2003 (first entry)
XX
DE Adjuvant-type CpG containing oligonucleotide #3.
XX
KW CpG island; ss; HIV infection; gene therapy; vaccine; B-cell;
KW immunostimulatory; adjuvant.
XX
OS Synthetic.
XX
PN US2003050263-A1.
XX
PD 13-MAR-2003.
XX
PF 16-AUG-2001; 2001US-00931583.
XX
PR 15-JUL-1994; 94US-00276358.
PR 07-FEB-1995; 95US-00386063.
PR 08-OCT-1999; 99US-00415142.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Klinman D, Steinberg AD;
XX
DR WPI; 2003-512356/48.
XX
PT Treating a subject infected with HIV by administering a CpG nucleic acid.
XX
PS Claim 50; Page 20; 22pp; English.
XX
CC The invention relates to treating a subject infected with HIV comprising
CC administering a CpG nucleic acid (e.g. an adjuvant type CpG
CC oligonucleotide, an immunostimulatory CpG oligonucleotide or a B cell
CC stimulatory CpG oligonucleotide). The CpG are used as gene therapy
CC vaccines to treat a subject infected with HIV. The present sequence is an
CC adjuvant type CpG oligonucleotide
XX
SQ Sequence 27 BP; 0 A; 4 C; 6 G; 17 T; 0 U; 0 Other;

Query Match 81.2%; Score 26; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26

RESULT 9
AAF99178
ID AAF99178 standard; DNA; 29 BP.
XX
AC AAF99178;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #294.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 44; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 29 BP; 0 A; 4 C; 6 G; 19 T; 0 U; 0 Other;

Query Match 81.2%; Score 26; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26

RESULT 10
ABS77821
ID ABS77821 standard; DNA; 29 BP.
XX
AC ABS77821;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #305.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 25; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 29 BP; 0 A; 4 C; 6 G; 19 T; 0 U; 0 Other;

Query Match 81.2%; Score 26; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26

RESULT 11
ABL38761
ID ABL38761 standard; DNA; 29 BP.
XX
AC ABL38761;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 131.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX

OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5' biotinylated"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 129; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 29 BP; 0 A; 4 C; 6 G; 19 T; 0 U; 0 Other;

```
  Query Match             81.2%;  Score 26;  DB 6;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
```

RESULT 12
ACD99609
ID ACD99609 standard; DNA; 29 BP.
XX
AC ACD99609;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #295.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 16; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 29 BP; 0 A; 4 C; 6 G; 19 T; 0 U; 0 Other;

```
  Query Match             81.2%;  Score 26;  DB 9;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
```

RESULT 13
ADB36680
ID ADB36680 standard; DNA; 29 BP.
XX
AC ADB36680;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #294.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.

```
XX
PS   Disclosure; Page 9; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 29 BP; 0 A; 4 C; 6 G; 19 T; 0 U; 0 Other;

  Query Match           81.2%;  Score 26;  DB 9;  Length 29;
  Best Local Similarity  100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26


RESULT 14
ADE39672
ID   ADE39672 standard; DNA; 48 BP.
XX
AC   ADE39672;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Oligonucleotide ODN 7 (INX-2006) SEQ ID NO:7.
XX
KW   cancer; vaccine; lipid-nucleic acid; LNA; tumour-associated antigen;
KW   Th-1 based immune response; cytostatic; gene therapy;
KW   tumour growth inhibition; tumour; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .48
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate linkages and
FT                   methylated cytosine residues"
XX
PN   WO2003094828-A2.
XX
PD   20-NOV-2003.
XX
PF   12-MAY-2003; 2003WO-CA000679.
XX
PR   10-MAY-2002; 2002US-0379343P.
PR   07-NOV-2002; 2002US-00290545.
PR   04-APR-2003; 2003US-0460646P.
XX
PA   (INEX-) INEX PHARM CORP.
XX
PI   Tam YK,  Semple S,  Klimuk S,  Chikh G;
XX
DR   WPI; 2004-011992/01.
XX
PT   New cancer vaccine having a lipid-nucleic acid formulation in combination
PT   with at least one tumor-associated antigen, useful for stimulating
PT   enhanced responses against tumor-associated antigens and for inhibiting
PT   tumor growth.
XX
PS   Example 9; SEQ ID NO 7; 119pp; English.
XX
CC   The present invention describes a cancer vaccine (I), which comprises a
CC   lipid-nucleic acid (LNA) formulation in combination with at least one
CC   tumour-associated antigen that is mixed with or associated with the LNA
CC   formulation comprising a lipid component having at least one cationic
CC   lipid, and a nucleic acid component comprising at least one
CC   oligonucleotide, where the vaccine is capable of stimulating a Th-1 based
CC   immune response in vivo to the at least one tumour-associated antigen.
CC   (I) has cytostatic activity, and can be used in vaccines, and in gene
CC   therapy. The methods and compositions of the present invention can be
CC   used for stimulating enhanced responses against tumour-associated
CC   antigens and for inhibiting tumour growth. The present sequence
CC   represents an oligonucleotide which is used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 48 BP; 0 A; 4 C; 12 G; 28 T; 0 U; 4 Other;

  Query Match           78.1%;  Score 25;  DB 12;  Length 48;
  Best Local Similarity  100.0%;  Pred. No. 0.00051;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTT 25
              |||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTT 25


RESULT 15
AAV83725
ID   AAV83725 standard; DNA; 52 BP.
XX
AC   AAV83725;
XX
DT   20-MAR-2003  (revised)
DT   15-MAR-1999  (first entry)
XX
DE   Plasmid pHIS CpG-S motif containing oligonucleotide.
XX
KW   CpG-N motif; immunostimulation; antigen; CpG-S motif; immunisation;
KW   viral antigen; bacterial antigen; parasite; therapeutic; growth factor;
KW   toxins; tumour suppressor; cytokine; apoptotic protein; interferon;
KW   hormone; clotting factor; ligand; receptor; ss.
XX
OS   Synthetic.
XX
PN   WO9852581-A1.
XX
PD   26-NOV-1998.
XX
PF   20-MAY-1998;   98WO-US010408.
XX
PR   20-MAY-1997;   97US-0047209P.
PR   20-MAY-1997;   97US-0047233P.
XX
PA   (OTTA-) OTTAWA CIVIC HOSPITAL LOEB RES INST.
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (QIAG-) QIAGEN GMBH.
XX
PI   Davis HL,  Krieg AM,  Schorr J,  Wu T;
XX
DR   WPI; 1999-059712/05.
XX
PT   Use of neutralising CpG and stimulating CpG motifs in DNA vectors - for
PT   enhancing the immunostimulatory effect of an antigen or enhancing the
PT   expression of a therapeutic polypeptide.
XX
PS   Example 1; Page 41; 109pp; English.
XX
CC   This sequence is used in the description of a method for enhancing the
CC   immunostimulatory effect of an antigen encoded by nucleic acid contained
CC   in a nucleic acid construct. The method involves determining the CpG-N
CC   and CpG-S motifs present in the construct, removing neutralising CpG (CpG
CC   -N) motifs and optionally inserting stimulatory CpG (CpG-S) motifs in the
CC   construct, thereby producing a nucleic acid construct having enhanced
CC   immunostimulatory efficacy. The method can be used for immunisation
CC   against viral antigens, e.g. from hepatitis B virus (HBV), bacterial
CC   antigens or an antigen derived from a parasite. They can also be used for
CC   expression of a therapeutic polypeptide, e.g. growth factors, toxins,
CC   tumour suppressors, cytokines, apoptotic proteins, interferons, hormones,
CC   clotting factors, ligands and receptors. (Updated on 20-MAR-2003 to
```

CC correct PA field.)
XX
SQ Sequence 52 BP; 1 A; 9 C; 14 G; 28 T; 0 U; 0 Other;

Query Match 78.1%; Score 25; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTT 25
              |||||||||||||||||||||||||
Db          4 TCGTCGTTTTGTCGTTTTGTCGTTT 28
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Search completed: February 14, 2005, 06:52:40
Job time : 298 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 06:47:45 ; Search time 302 Seconds
(without alignments)
625.214 Million cell updates/sec

Title: US-10-076-674A-1
Perfect score: 32
Sequence: 1 tcgtcgttttgtcgttttgtcgttttgtcgtt 32

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5378673 seqs, 2950229984 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5029582

Minimum DB seq length: 0
Maximum DB seq length: 64

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	32	10	US-09-888-326-734	Sequence 734, App
2	32	100.0	32	10	US-09-776-479-429	Sequence 429, App
3	32	100.0	32	11	US-09-776-479-429	Sequence 429, App
4	32	100.0	32	14	US-10-112-653-411	Sequence 411, App
5	32	100.0	32	14	US-10-017-995-429	Sequence 429, App
6	32	100.0	32	16	US-10-076-674-1	Sequence 1, Appli
7	32	100.0	32	17	US-10-314-578-429	Sequence 429, App
8	32	100.0	32	17	US-10-355-161A-1	Sequence 1, Appli
9	32	100.0	32	18	US-10-831-778-429	Sequence 429, App
10	26	81.2	27	10	US-09-931-583-35	Sequence 35, Appl
11	26	81.2	29	10	US-09-888-326-131	Sequence 131, App
12	26	81.2	29	10	US-09-776-479-305	Sequence 305, App
13	26	81.2	29	11	US-09-776-479-305	Sequence 305, App
14	26	81.2	29	14	US-10-112-653-295	Sequence 295, App
15	26	81.2	29	14	US-10-017-995-305	Sequence 305, App
16	26	81.2	29	17	US-10-314-578-305	Sequence 305, App
17	26	81.2	29	18	US-10-831-778-305	Sequence 305, App
18	25	78.1	52	11	US-09-965-101-15	Sequence 15, Appl
19	24	75.0	24	9	US-09-760-506-4	Sequence 4, Appli
20	24	75.0	24	9	US-09-768-012-4	Sequence 4, Appli
21	24	75.0	24	9	US-09-824-468-90	Sequence 90, Appl
22	24	75.0	24	9	US-09-800-266A-77	Sequence 77, Appl
23	24	75.0	24	9	US-09-895-007A-77	Sequence 77, Appl
24	24	75.0	24	9	US-09-920-313-77	Sequence 77, Appl
25	24	75.0	24	9	US-09-920-313-147	Sequence 147, App
26	24	75.0	24	10	US-09-927-422A-23	Sequence 23, Appl
27	24	75.0	24	10	US-09-888-326-729	Sequence 729, App
28	24	75.0	24	10	US-09-888-326-730	Sequence 730, App
29	24	75.0	24	10	US-09-888-326-731	Sequence 731, App
30	24	75.0	24	10	US-09-888-326-732	Sequence 732, App
31	24	75.0	24	10	US-09-888-326-733	Sequence 733, App
32	24	75.0	24	10	US-09-931-583-29	Sequence 29, Appl
33	24	75.0	24	10	US-09-931-583-38	Sequence 38, Appl
34	24	75.0	24	10	US-09-931-583-68	Sequence 68, Appl
35	24	75.0	24	10	US-09-927-884-14	Sequence 14, Appl
36	24	75.0	24	10	US-09-776-479-246	Sequence 246, App
37	24	75.0	24	10	US-09-776-479-262	Sequence 262, App
38	24	75.0	24	10	US-09-776-479-273	Sequence 273, App
39	24	75.0	24	10	US-09-776-479-300	Sequence 300, App
40	24	75.0	24	10	US-09-776-479-352	Sequence 352, App
41	24	75.0	24	10	US-09-776-479-412	Sequence 412, App
42	24	75.0	24	10	US-09-776-479-413	Sequence 413, App
43	24	75.0	24	10	US-09-776-479-964	Sequence 964, App
44	24	75.0	24	10	US-09-776-479-965	Sequence 965, App
45	24	75.0	24	10	US-09-776-479-966	Sequence 966, App

ALIGNMENTS

RESULT 1
US-09-888-326-734
; Sequence 734, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 734
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-734

Query Match 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 2
US-09-776-479-429
; Sequence 429, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 429
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-429

Query Match 100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 3
US-09-776-479-429
; Sequence 429, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 429
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-429

Query Match 100.0%; Score 32; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 4
US-10-112-653-411
; Sequence 411, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 411
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-411

Query Match 100.0%; Score 32; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 5
US-10-017-995-429
; Sequence 429, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 429
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-429

Query Match 100.0%; Score 32; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 6
US-10-076-674-1
; Sequence 1, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-076-674-1

Query Match 100.0%; Score 32; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 7
US-10-314-578-429
; Sequence 429, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 429
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-429

Query Match 100.0%; Score 32; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 8
US-10-355-161A-1
; Sequence 1, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-355-161A-1

Query Match 100.0%; Score 32; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 9
US-10-831-778-429
; Sequence 429, Application US/10831778
; Publication No. US20040235774A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/831,778
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 429
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-831-778-429

Query Match 100.0%; Score 32; DB 18; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
||||||||||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 10
US-09-931-583-35
; Sequence 35, Application US/09931583
; Publication No. US20030050263A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur
; APPLICANT: Klinman, Dennis
; APPLICANT: Steinberg, Alfred
; TITLE OF INVENTION: Methods and Products for Treating HIV Infection
; FILE REFERENCE: C1039/7053(HCL)
; CURRENT APPLICATION NUMBER: US/09/931,583
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; PRIOR APPLICATION NUMBER: US 09/415,142
; PRIOR FILING DATE: 1999-10-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-931-583-35

```
  Query Match           81.2%;  Score 26;  DB 10;  Length 27;
  Best Local Similarity 100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
```

```
RESULT 11
US-09-888-326-131
; Sequence 131, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 131
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
;   OTHER INFORMATION: with phosphodiester on 5' end
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: biotinylated at 5' end
US-09-888-326-131
```

```
  Query Match           81.2%;  Score 26;  DB 10;  Length 29;
  Best Local Similarity 100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
```

```
RESULT 12
US-09-776-479-305
; Sequence 305, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 305
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(3)
;   OTHER INFORMATION: Conjugated to biotin moiety.
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-305
```

```
  Query Match           81.2%;  Score 26;  DB 10;  Length 29;
  Best Local Similarity 100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
```

```
RESULT 13
US-09-776-479-305
; Sequence 305, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  APPLICANT:  Petersen, Deanna M.
;  APPLICANT:  Fouron, Yves
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
;  TITLE OF INVENTION:  Treatment of Asthma and Allergy
;  FILE REFERENCE: C1037/7013 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/776,479
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: US 60/179,991
;  PRIOR FILING DATE: 2000-02-03
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 305
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(3)
;   OTHER INFORMATION: Conjugated to biotin moiety.
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-776-479-305
```

```
  Query Match           81.2%;  Score 26;  DB 11;  Length 29;
  Best Local Similarity 100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
```

```
RESULT 14
US-10-112-653-295
; Sequence 295, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 295
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Synthetic Oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: biotinylated
US-10-112-653-295

  Query Match             81.2%;  Score 26;  DB 14;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26


RESULT 15
US-10-017-995-305
; Sequence 305, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
;  PRIOR APPLICATION NUMBER: US 60/255,534
;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 305
;   LENGTH: 29
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(3)
;   OTHER INFORMATION: Conjugated to biotin moiety.
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-305

  Query Match             81.2%;  Score 26;  DB 14;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 0.00016;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26


Search completed: February 14, 2005, 09:34:33
Job time : 303 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 06:20:39 ; Search time 102 Seconds
(without alignments)
513.342 Million cell updates/sec

Title: US-10-076-674A-1
Perfect score: 32
Sequence: 1 tcgtcgttttgtcgttttgtcgttttgtcgtt 32

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1260380

Minimum DB seq length: 0
Maximum DB seq length: 64

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25	78.1	52	3	US-09-082-649B-15	Sequence 15, Appl
2	25	78.1	52	4	US-09-965-101-15	Sequence 15, Appl
3	24	75.0	24	3	US-09-030-701-6	Sequence 6, Appli
4	24	75.0	24	3	US-09-286-098-90	Sequence 90, Appl
5	24	75.0	24	3	US-08-960-774-46	Sequence 46, Appl
6	24	75.0	24	3	US-09-082-649B-3	Sequence 3, Appli
7	24	75.0	24	3	US-09-082-649B-66	Sequence 66, Appl
8	24	75.0	24	3	US-09-325-193A-77	Sequence 77, Appl
9	24	75.0	24	3	US-09-191-170-84	Sequence 84, Appl
10	24	75.0	24	3	US-09-191-170-95	Sequence 95, Appl
11	24	75.0	24	4	US-09-690-921-4	Sequence 4, Appli
12	24	75.0	24	4	US-09-337-619-46	Sequence 46, Appl
13	24	75.0	24	4	US-09-965-101-3	Sequence 3, Appli
14	24	75.0	24	4	US-09-965-101-66	Sequence 66, Appl
15	23	71.9	23	4	US-09-337-619-123	Sequence 123, App
16	16	50.0	22	3	US-09-030-701-8	Sequence 8, Appli
17	16	50.0	22	3	US-09-286-098-91	Sequence 91, Appl
18	16	50.0	22	3	US-08-960-774-49	Sequence 49, Appl
19	16	50.0	22	3	US-09-082-649B-67	Sequence 67, Appl
20	16	50.0	22	3	US-09-325-193A-78	Sequence 78, Appl
21	16	50.0	22	3	US-09-191-170-85	Sequence 85, Appl
22	16	50.0	22	4	US-09-337-619-49	Sequence 49, Appl
23	16	50.0	22	4	US-09-965-101-67	Sequence 67, Appl
c 24	11	34.4	18	3	US-09-513-783A-127	Sequence 127, App
c 25	11	34.4	18	4	US-09-430-656-127	Sequence 127, App
c 26	11	34.4	25	3	US-08-564-110C-5	Sequence 5, Appli
27	11	34.4	25	4	US-09-396-196G-19324	Sequence 19324, A
c 28	11	34.4	28	3	US-09-359-753A-20	Sequence 20, Appl
29	11	34.4	28	3	US-09-359-753A-21	Sequence 21, Appl
c 30	11	34.4	29	4	US-09-086-118-6	Sequence 6, Appli
c 31	11	34.4	30	1	US-07-931-473B-29	Sequence 29, Appl
c 32	11	34.4	30	1	US-07-714-131C-29	Sequence 29, Appl
c 33	11	34.4	30	1	US-08-412-110-29	Sequence 29, Appl
c 34	11	34.4	30	1	US-08-409-442A-29	Sequence 29, Appl
c 35	11	34.4	30	2	US-08-469-609A-29	Sequence 29, Appl
c 36	11	34.4	30	3	US-09-143-190-29	Sequence 29, Appl
c 37	11	34.4	30	3	US-09-502-344-29	Sequence 29, Appl
c 38	11	34.4	30	3	US-09-648-040-3	Sequence 3, Appli
39	11	34.4	37	1	US-08-495-743-21	Sequence 21, Appl
40	11	34.4	37	1	US-08-495-739-21	Sequence 21, Appl
41	11	34.4	37	1	US-08-495-741-21	Sequence 21, Appl
42	11	34.4	37	3	US-08-062-023-21	Sequence 21, Appl
43	11	34.4	39	1	US-08-049-473-22	Sequence 22, Appl
44	11	34.4	39	1	US-08-312-648-22	Sequence 22, Appl
45	11	34.4	39	5	PCT-US94-04190-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-082-649B-15
; Sequence 15, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7009
; CURRENT APPLICATION NUMBER: US/09/082,649B
; CURRENT FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-15

Query Match 78.1%; Score 25; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTT 25
||||||||||||||||||||||||||
Db 4 TCGTCGTTTTGTCGTTTTGTCGTTT 28

RESULT 2
US-09-965-101-15
; Sequence 15, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schorr, Joachim
; APPLICANT: Wu, Tong
; TITLE OF INVENTION: Vectors and Methods for Immunization or
; TITLE OF INVENTION: Therapeutic Protocols
; FILE REFERENCE: C1039/7057 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/965,101

; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 09/082,649
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 60/047,233
; PRIOR FILING DATE: 1997-05-20
; PRIOR APPLICATION NUMBER: US 60/047,209
; PRIOR FILING DATE: 1997-05-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-965-101-15

Query Match 78.1%; Score 25; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTT 25
||||||||||||||||||||||||||
Db 4 TCGTCGTTTTGTCGTTTTGTCGTTT 28

RESULT 3
US-09-030-701-6
; Sequence 6, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CpG DINUCLEOTIDE IN THE TREATMENT OF
; TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-6

Query Match 75.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTT 24
||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTT 24

RESULT 4
US-09-286-098-90
, Sequence 90, Application US/09286098
, Patent No. 6218371
, GENERAL INFORMATION:
, APPLICANT: Krieg, Arthur M.
, APPLICANT: Weiner, George
, TITLE OF INVENTION: Methods and Products for Stimulating the
, TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
, TITLE OF INVENTION: Cytokines
, FILE REFERENCE: C1039/7026/HCL
, CURRENT APPLICATION NUMBER: US/09/286,098
, CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-90

Query Match 75.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTT 24
||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTT 24

RESULT 5
US-08-960-774-46
; Sequence 46, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieg et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-960-774-46

Query Match 75.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTT 24
||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTT 24

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RESULT 6
US-09-082-649B-3
; Sequence 3, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
;  APPLICANT:  Davis, Heather L.
;  APPLICANT:  Krieg, Arthur M.
;  APPLICANT:  Schorr, Joachim
;  APPLICANT:  Wu, Tong
;  TITLE OF INVENTION:  Vectors and Methods for Immunization or
;  TITLE OF INVENTION:  Therapeutic Protocols
;  FILE REFERENCE:  C1039/7009
;  CURRENT APPLICATION NUMBER: US/09/082,649B
;  CURRENT FILING DATE:  1998-05-20
;  PRIOR APPLICATION NUMBER:  US 60/047,233
;  PRIOR FILING DATE:  1997-05-20
;  PRIOR APPLICATION NUMBER:  US 60/047,209
;  PRIOR FILING DATE:  1997-05-20
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-082-649B-3

  Query Match             75.0%;  Score 24;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 7
US-09-082-649B-66
; Sequence 66, Application US/09082649B
; Patent No. 6339068
; GENERAL INFORMATION:
;  APPLICANT:  Davis, Heather L.
;  APPLICANT:  Krieg, Arthur M.
;  APPLICANT:  Schorr, Joachim
;  APPLICANT:  Wu, Tong
;  TITLE OF INVENTION:  Vectors and Methods for Immunization or
;  TITLE OF INVENTION:  Therapeutic Protocols
;  FILE REFERENCE:  C1039/7009
;  CURRENT APPLICATION NUMBER: US/09/082,649B
;  CURRENT FILING DATE:  1998-05-20
;  PRIOR APPLICATION NUMBER:  US 60/047,233
;  PRIOR FILING DATE:  1997-05-20
;  PRIOR APPLICATION NUMBER:  US 60/047,209
;  PRIOR FILING DATE:  1997-05-20
;  NUMBER OF SEQ ID NOS:  85
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 66
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Backbone is a phosphorothioate--phosphodiester
;   OTHER INFORMATION: chimera.
US-09-082-649B-66

  Query Match             75.0%;  Score 24;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
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Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 8
US-09-325-193A-77
; Sequence 77, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
;  APPLICANT:  Davis, Heather L.
;  APPLICANT:  Schorr, Joachim
;  APPLICANT:  Krieg, Arthur M.
;  TITLE OF INVENTION:  Use of Nucleic Acids Containing
;  TITLE OF INVENTION:  Unmethylated CpG Dinucleotide as an Adjuvant
;  FILE REFERENCE:  C1039/7025/HCL
;  CURRENT APPLICATION NUMBER: US/09/325,193A
;  CURRENT FILING DATE:  1999-06-03
;  PRIOR APPLICATION NUMBER:  US 09/154,614
;  PRIOR FILING DATE:  1998-09-16
;  PRIOR APPLICATION NUMBER:  PCT/US98/04703
;  PRIOR FILING DATE:  1998-03-10
;  PRIOR APPLICATION NUMBER:  US 60/040,376
;  PRIOR FILING DATE:  1997-03-10
;  NUMBER OF SEQ ID NOS:  98
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 77
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-77

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  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
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Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 9
US-09-191-170-84
; Sequence 84, Application US/09191170
; Patent No. 6429199
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT: Hartmann, Gunther
;  TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
;  TITLE OF INVENTION: for Activating Dendritic Cells
;  FILE REFERENCE: C1039/7017
;  CURRENT APPLICATION NUMBER: US/09/191,170
;  CURRENT FILING DATE: 1998-11-13
;  EARLIER APPLICATION NUMBER: US 08/960,774
;  EARLIER FILING DATE: 1997-10-30
;  EARLIER APPLICATION NUMBER: US 08/738,652
;  EARLIER FILING DATE: 1996-10-30
;  EARLIER APPLICATION NUMBER: US 08/386,063
;  EARLIER FILING DATE: 1995-02-07
;  EARLIER APPLICATION NUMBER: US 08/276,358
;  EARLIER FILING DATE: 1994-07-15
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 84
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-191-170-84

Query Match 75.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTT 24
||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTT 24

RESULT 10
US-09-191-170-95
; Sequence 95, Application US/09191170
; Patent No. 6429199
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; TITLE OF INVENTION: for Activating Dendritic Cells
; FILE REFERENCE: C1039/7017
; CURRENT APPLICATION NUMBER: US/09/191,170
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2)...(2)
; OTHER INFORMATION: m5c
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (5)...(5)
; OTHER INFORMATION: m5c
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)...(13)
; OTHER INFORMATION: m5c
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (21)...(21)
; OTHER INFORMATION: m5c
US-09-191-170-95

Query Match 75.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTT 24
||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTT 24

RESULT 11
US-09-690-921-4
; Sequence 4, Application US/09690921
; Patent No. 6544518
; GENERAL INFORMATION:
; APPLICANT: Friede, Martin
; APPLICANT: Gerard, Catherine
; APPLICANT: Hermand, Philippe
; TITLE OF INVENTION: Vaccines
; FILE REFERENCE: B45181-1
; CURRENT APPLICATION NUMBER: US/09/690,921
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/EP00/02920
; PRIOR FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/301,829
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 9908885.8
; PRIOR FILING DATE: 1999-04-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Human
US-09-690-921-4

Query Match 75.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTT 24
||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTT 24

RESULT 12
US-09-337-619-46
; Sequence 46, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Methods of Treating Cancer Using
; TITLE OF INVENTION: Immunostimulatory Oligonucleotides
; FILE REFERENCE: C1039/7021/HCL
; CURRENT APPLICATION NUMBER: US/09/337,619
; CURRENT FILING DATE: 1999-06-21
; EARLIER APPLICATION NUMBER: US 08/960,774
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: US 08/738,652
; EARLIER FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-46

Query Match 75.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTT 24
||||||||||||||||||||||||
Db 1 TCGTCGTTTTGTCGTTTTGTCGTT 24

RESULT 13
US-09-965-101-3
; Sequence 3, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:

```
;  APPLICANT: Davis, Heather L.
;  APPLICANT:  Krieg, Arthur M.
;  APPLICANT:  Schorr, Joachim
;  APPLICANT:  Wu, Tong
;  TITLE OF INVENTION: Vectors and Methods for Immunization or
;  TITLE OF INVENTION:  Therapeutic Protocols
;  FILE REFERENCE: C1039/7057 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/965,101
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: US 09/082,649
;  PRIOR FILING DATE: 1998-05-20
;  PRIOR APPLICATION NUMBER: US 60/047,233
;  PRIOR FILING DATE: 1997-05-20
;  PRIOR APPLICATION NUMBER: US 60/047,209
;  PRIOR FILING DATE: 1997-05-20
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Has a phosphorothioate backbone.
US-09-965-101-3

  Query Match             75.0%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 14
US-09-965-101-66
; Sequence 66, Application US/09965101
; Patent No. 6821957
; GENERAL INFORMATION:
;  APPLICANT: Davis, Heather L.
;  APPLICANT:  Krieg, Arthur M.
;  APPLICANT:  Schorr, Joachim
;  APPLICANT:  Wu, Tong
;  TITLE OF INVENTION: Vectors and Methods for Immunization or
;  TITLE OF INVENTION:  Therapeutic Protocols
;  FILE REFERENCE: C1039/7057 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/965,101
;  CURRENT FILING DATE:  2001-09-26
;  PRIOR APPLICATION NUMBER: US 09/082,649
;  PRIOR FILING DATE: 1998-05-20
;  PRIOR APPLICATION NUMBER: US 60/047,233
;  PRIOR FILING DATE: 1997-05-20
;  PRIOR APPLICATION NUMBER: US 60/047,209
;  PRIOR FILING DATE: 1997-05-20
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 66
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Backbone is a phosphorothioate--phosphodiester
;   OTHER INFORMATION: chimera.
US-09-965-101-66

  Query Match             75.0%;  Score 24;  DB 4;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00042;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 15
US-09-337-619-123
; Sequence 123, Application US/09337619
; Patent No. 6653292
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  TITLE OF INVENTION: Methods of Treating Cancer Using
;  TITLE OF INVENTION: Immunostimulatory Oligonucleotides
;  FILE REFERENCE: C1039/7021/HCL
;  CURRENT APPLICATION NUMBER: US/09/337,619
;  CURRENT FILING DATE: 1999-06-21
;  EARLIER APPLICATION NUMBER: US 08/960,774
;  EARLIER FILING DATE: 1997-10-30
;  EARLIER APPLICATION NUMBER: US 08/738,652
;  EARLIER FILING DATE: 1996-10-30
;  EARLIER APPLICATION NUMBER: US 08/386,063
;  EARLIER FILING DATE: 1995-02-07
;  EARLIER APPLICATION NUMBER: US 08/276,358
;  EARLIER FILING DATE: 1994-07-15
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 123
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-09-337-619-123

  Query Match             71.9%;  Score 23;  DB 4;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.0014;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGT 23
              |||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGT 23


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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	32	6	AX104237	AX104237 Sequence
2	32	100.0	32	6	AX355706	AX355706 Sequence
3	32	100.0	32	6	AX547290	AX547290 Sequence
4	26	81.2	29	6	AX104113	AX104113 Sequence
5	26	81.2	29	6	AX355103	AX355103 Sequence
6	26	81.2	29	6	AX547166	AX547166 Sequence
7	25	78.1	52	6	AR182843	AR182843 Sequence
8	24	75.0	24	6	AR146378	AR146378 Sequence
9	24	75.0	24	6	AR154717	AR154717 Sequence
10	24	75.0	24	6	BD205600	BD205600 Method of
11	24	75.0	24	6	BD261142	BD261142 Methods a
12	24	75.0	24	6	BD261298	BD261298 Methods a
13	24	75.0	24	6	BD261563	BD261563 Vaccine.
14	24	75.0	24	6	BD267904	BD267904 Methods f
15	24	75.0	24	6	BD270804	BD270804 Stereoiso
16	24	75.0	24	6	CQ769070	CQ769070 Sequence
17	24	75.0	24	6	CQ788116	CQ788116 Sequence
18	24	75.0	24	6	CQ788202	CQ788202 Sequence
19	24	75.0	24	6	CQ815138	CQ815138 Sequence
20	24	75.0	24	6	CQ875565	CQ875565 Sequence
21	24	75.0	24	6	AR182831	AR182831 Sequence
22	24	75.0	24	6	AR182894	AR182894 Sequence
23	24	75.0	24	6	AR213877	AR213877 Sequence
24	24	75.0	24	6	AR222250	AR222250 Sequence
25	24	75.0	24	6	AR222261	AR222261 Sequence
26	24	75.0	24	6	AR303121	AR303121 Sequence
27	24	75.0	24	6	AR432469	AR432469 Sequence
28	24	75.0	24	6	AX040171	AX040171 Sequence
29	24	75.0	24	6	AX045771	AX045771 Sequence
30	24	75.0	24	6	AX045776	AX045776 Sequence
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35	24	75.0	24	6	AX045786	AX045786 Sequence
36	24	75.0	24	6	AX045789	AX045789 Sequence
37	24	75.0	24	6	AX104054	AX104054 Sequence
38	24	75.0	24	6	AX104070	AX104070 Sequence
39	24	75.0	24	6	AX104081	AX104081 Sequence
40	24	75.0	24	6	AX104108	AX104108 Sequence
41	24	75.0	24	6	AX104160	AX104160 Sequence
42	24	75.0	24	6	AX104220	AX104220 Sequence
43	24	75.0	24	6	AX104221	AX104221 Sequence
44	24	75.0	24	6	AX104772	AX104772 Sequence
45	24	75.0	24	6	AX104773	AX104773 Sequence

ALIGNMENTS

RESULT 1
AX104237
LOCUS AX104237 32 bp DNA linear PAT 01-MAY-2001
DEFINITION Sequence 429 from Patent WO0122972.
ACCESSION AX104237
VERSION AX104237.1 GI:13920434
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 429 05-APR-2001
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
source 1. .32
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 32; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
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Db 1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32

RESULT 2
AX355706
LOCUS AX355706 32 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 734 from Patent WO0197843.
ACCESSION AX355706
VERSION AX355706.1 GI:18620374
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

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REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 734 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide~phosphorothioate
                     backbone"
ORIGIN

  Query Match           100.0%;  Score 32;  DB 6;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-08;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
              ||||||||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32


RESULT 3
AX547290
LOCUS       AX547290                 32 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 429 from Patent WO02053141.
ACCESSION   AX547290
VERSION     AX547290.1  GI:25812434
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 429 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
ORIGIN

  Query Match           100.0%;  Score 32;  DB 6;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-08;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32
              ||||||||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTTGTCGTT 32


RESULT 4
AX104113
LOCUS       AX104113                 29 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 305 from Patent WO0122972.
ACCESSION   AX104113
VERSION     AX104113.1  GI:13920310
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 305 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .3
                     /note="Biotin moiety attached at 5' end of sequence."
ORIGIN

  Query Match           81.2%;  Score 26;  DB 6;  Length 29;
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  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26


RESULT 5
AX355103
LOCUS       AX355103                 29 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 131 from Patent WO0197843.
ACCESSION   AX355103
VERSION     AX355103.1  GI:18619770
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 131 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide~chimeric
                     phosphorothioate/phosphodiester backbone with
                     phosphodiester on 5' end"
     misc_feature    1
                     /note="biotinylated at 5' end"
ORIGIN

  Query Match           81.2%;  Score 26;  DB 6;  Length 29;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-05;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26


RESULT 6
AX547166
LOCUS       AX547166                 29 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 305 from Patent WO02053141.
ACCESSION   AX547166
VERSION     AX547166.1  GI:25812310
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 305 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .29
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                     /note="Conjugated to biotin moiety.
                     Synthetic Sequence"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26
              ||||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTTTT 26


RESULT 7
AR182843
LOCUS       AR182843                 52 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 15 from patent US 6339068.
ACCESSION   AR182843
VERSION     AR182843.1  GI:20226050
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Krieg,A.M., Davis,H.L., Wu,T. and Schorr,J.
  TITLE     Vectors and methods for immunization or therapeutic protocols
  JOURNAL   Patent: US 6339068-A 15 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .52
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ORIGIN

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Qy          1 TCGTCGTTTTGTCGTTTTGTCGTTT 25
              |||||||||||||||||||||||||
Db          4 TCGTCGTTTTGTCGTTTTGTCGTTT 28


RESULT 8
AR146378
LOCUS       AR146378                 24 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 90 from patent US 6218371.
ACCESSION   AR146378
VERSION     AR146378.1  GI:15109567
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Krieg,A.M. and Weiner,G.
  TITLE     Methods and products for stimulating the immune system using
            immunotherapeutic oligonucleotides and cytokines
  JOURNAL   Patent: US 6218371-A 90 17-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .24
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ORIGIN

  Query Match             75.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00066;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
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Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 9
AR154717
LOCUS       AR154717                 24 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 46 from patent US 6239116.
ACCESSION   AR154717
VERSION     AR154717.1  GI:15122770
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Krieg,A.M. and Kline,J.N.
  TITLE     Immunostimulatory nucleic acid molecules
  JOURNAL   Patent: US 6239116-A 46 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .24
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             75.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00066;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 10
BD205600
LOCUS       BD205600                 24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of controlling hematopoiesis by using CpG oligonucleotide.
ACCESSION   BD205600
VERSION     BD205600.1  GI:33015370
KEYWORDS    JP 2002514397-A/90.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Wagner,H. and Lipford,G.
  TITLE     Method of controlling hematopoiesis by using CpG oligonucleotide
  JOURNAL   Patent: JP 2002514397-A 90 21-MAY-2002;
            CORY PHARMACEUTICALS GMBH,CORY PHARMACEUTICALS GROUP INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002514397-A/90
            PD   21-MAY-2002
            PF   14-MAY-1999 JP 2000547969
            PR   14-MAY-1998 US    60/085516,02-FEB-1999 US    09/241653 PI
            HERMANN WAGNER,GRAYSON LIPFORD
            PC   C12N15/09,A61K31/70,A61K39/39,C07H21/04//A61K45/00,C12N15/00
            CC   Synthetic Sequence
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
     source          1. .24
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             75.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00066;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 11
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BD261142
LOCUS       BD261142                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methods and products for stimulating the immune system using
            immunotherapeutic oligonucleotides and cytokines.
ACCESSION   BD261142
VERSION     BD261142.1  GI:33070912
KEYWORDS    JP 2002510644-A/90.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Krieg,A.M. and Weiner,G.
  TITLE     Methods and products for stimulating the immune system using
            immunotherapeutic oligonucleotides and cytokines
  JOURNAL   Patent: JP 2002510644-A 90 09-APR-2002;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT     OS   Artificial Sequence
            PN   JP 2002510644-A/90
            PD   09-APR-2002
            PF   02-APR-1999 JP 2000542030
            PR   03-APR-1998 US    60/080729
            PI   ARTHUR M KRIEG,GEORGE WEINER
            PC   A61K38/00,A61K31/7088,A61K39/00,A61P15/00,A61P35/00,A61P37/04,
            PC   A61K37/02
            CC   Synthetic Sequence
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
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ORIGIN

  Query Match             75.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00066;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 12
BD261298
LOCUS       BD261298                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methods and products for inducing mucosal immunity.
ACCESSION   BD261298
VERSION     BD261298.1  GI:33071068
KEYWORDS    JP 2002516294-A/77.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Mccluskie,M.J. and Davis,H.L.
  TITLE     Methods and products for inducing mucosal immunity
  JOURNAL   Patent: JP 2002516294-A 77 04-JUN-2002;
            LOEB HEALTH RESEARCH INSTITUTE AT THE OTTAWA HOSPITAL, CORY
            PHARMACEUTICALS GROUP INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002516294-A/77
            PD   04-JUN-2002
            PF   21-MAY-1999 JP 2000550515
            PR   22-MAY-1998 US    60/086393
            PI   MICHAEL J MCCLUSKIE,HEATHER L DAVIS
            PC
            A61K39/00,A61K9/10,A61K9/16,A61K9/50,A61K9/51,A61K31/70,A61K39/ PC
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            PC   A61P31/00,A61P35/00,A61P37/00
            CC   immunostimulatory synthetic oligonucleotide
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0.00066;
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Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 13
BD261563
LOCUS       BD261563                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Vaccine.
ACCESSION   BD261563
VERSION     BD261563.1  GI:33071331
KEYWORDS    JP 2002542203-A/4.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Friede,M., Garcon,N. and Hermand,P.
  TITLE     Vaccine
  JOURNAL   Patent: JP 2002542203-A 4 10-DEC-2002;
            SMITHKLINE BEECHAM BIOLOGICALS SA
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002542203-A/4
            PD   10-DEC-2002
            PF   04-APR-2000 JP 2000611936
            PR   19-APR-1999 GB    9908885.8,29-APR-1999 US    09/301829 PI
            MARTIN FRIEDE,NATHALIE GARCON,PHILIPPE HERMAND PC
            A61K39/39,A61K31/7088,A61K39/00,A61K39/00,A61K39/00,A61K39/02, PC
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            PC   145,A61K39/21,
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ORIGIN

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Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 14
BD267904
LOCUS       BD267904                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methods for the prevention and treatment of parasitic infections
            and related diseases using CPG oligonucleotides.
```

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ACCESSION   BD267904
VERSION     BD267904.1  GI:33077672
KEYWORDS    JP 2002513763-A/77.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Gramzinski,R.A., Krieg,A.M., Davis,H.L. and Hoffman,S.L.
  TITLE     Methods for the prevention and treatment of parasitic infections
            and related diseases using CPG oligonucleotides
  JOURNAL   Patent: JP 2002513763-A 77 14-MAY-2002;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION, OTTAWA CIVIC LOEB RESEARCH
            INSTITUTE, UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY
            OF THE NAVY
COMMENT     OS   Artificial Sequence
            PN   JP 2002513763-A/77
            PD   14-MAY-2002
            PF   06-MAY-1999 JP 2000546780
            PR   06-MAY-1998 US    60/084512
            PI   ROBERT A GRAMZINSKI,ARTHUR M KRIEG,HEATHER L DAVIS,STEPHEN L
            PI   HOFFMAN
            PC   A61K31/711,A61K9/127,A61K38/00,A61K38/22,A61K45/00,A61P31/00,
            PC   A61P33/00//
            PC   C12N15/09,A61K37/02,A61K37/24,C12N15/00
            CC   Synthetic Sequence
            FH   Key             Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0.00066;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
              ||||||||||||||||||||||||
Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


RESULT 15
BD270804
LOCUS       BD270804                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Stereoisomer of CpG oligonucleotide and method relating thereto.
ACCESSION   BD270804
VERSION     BD270804.1  GI:33080572
KEYWORDS    JP 2002521489-A/77.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Krieg,A.M.
  TITLE     Stereoisomer of CpG oligonucleotide and method relating thereto
  JOURNAL   Patent: JP 2002521489-A 77 16-JUL-2002;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT     OS   Artificial Sequence
            PN   JP 2002521489-A/77
            PD   16-JUL-2002
            PF   27-JUL-1999 JP 2000562385
            PR   27-JUL-1998 US    60/094370
            PI   ARTHUR M KRIEG
            PC   A61K31/711,A61P11/06,A61P17/00,A61P27/02,A61P29/00,A61P31/00,
            PC   A61P31/00,
            PC   A61P35/00,A61P37/04,A61P37/06,A61P37/08
            CC   Synthetic
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             75.0%;  Score 24;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00066;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGTCGTTTTGTCGTT 24
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Db          1 TCGTCGTTTTGTCGTTTTGTCGTT 24


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 06:22:14 ; Search time 7557 Seconds
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Title: US-10-076-674A-1
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 4	12	37.5	34	9	AJ595925	AJ595925 Arabidops
5	12	37.5	47	8	BH863768	BH863768 SALK_0945
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7	12	37.5	50	8	AZ472468	AZ472468 1M0287P08
8	12	37.5	56	9	BX286679	BX286679 Arabidops
9	12	37.5	57	9	AL754515	AL754515 Arabidops
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12	12	37.5	63	6	CB064048	CB064048 py03c06.y
13	12	37.5	63	6	CB192029	CB192029 py23h12.y
14	12	37.5	64	6	CB191498	CB191498 py32h10.y
15	11	34.4	23	8	BH848405	BH848405 SALK_0681
16	11	34.4	39	8	BH790795	BH790795 SALK_0579
17	11	34.4	42	8	BH864623	BH864623 SALK_0963
18	11	34.4	42	8	BH906749	BH906749 SALK_0356
c 19	11	34.4	43	8	BH856940	BH856940 SALK_0775
20	11	34.4	43	8	BZ665236	BZ665236 SALK_1109
c 21	11	34.4	43	8	BZ768681	BZ768681 SALK_1405
c 22	11	34.4	43	8	BZ768688	BZ768688 SALK_1405
c 23	11	34.4	43	8	BZ768713	BZ768713 SALK_1406
c 24	11	34.4	46	8	BH905634	BH905634 SALK_1075
c 25	11	34.4	49	8	BH865521	BH865521 SALK_0987
c 26	11	34.4	51	8	BH905632	BH905632 SALK_1075
c 27	11	34.4	51	9	CR141214	CR141214 Forward s
c 28	11	34.4	52	1	AI018533	AI018533 ou24h06.x
c 29	11	34.4	52	7	CN867563	CN867563 001118AAN
30	11	34.4	52	8	BZ664403	BZ664403 SALK_0709
c 31	11	34.4	55	1	AI689325	AI689325 tx93h03.x
c 32	11	34.4	55	8	BH903699	BH903699 SALK_1031
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36	11	34.4	57	9	CC886625	CC886625 SALK_1488
37	11	34.4	58	6	CD746336	CD746336 S30_G12_S
c 38	11	34.4	60	7	D18668	D18668 MUSGS01730
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c 40	11	34.4	61	8	BH905586	BH905586 SALK_1069
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42	10	31.2	26	8	AZ312531	AZ312531 1M0028J21
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ALIGNMENTS

RESULT 1
AL756165/c
LOCUS AL756165 38 bp DNA linear GSS 31-MAR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-106B12-012499, genomic survey sequence.
ACCESSION AL756165
VERSION AL756165.1 GI:21488663
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 38)
AUTHORS Strizhov,N., Rosso,M.G., Li,Y. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the right border of the T-DNA. Details on the protocols used for generation of the sequence are described in References 1-3. Re-examination of the source from which this sequence has been produced indicates that the sequence is of low reliability. Therefore, no information on a potential insertion site is deduced. The sequences are generated at the MPI

for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source Location/Qualifiers
1. .38
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-106B12-012499"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 43.8%; Score 14; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTTTGTCGTTTTGT 20
||||||||||||||
Db 29 TTTTGTCGTTTTGT 16

RESULT 2
BQ613522/c
LOCUS BQ613522 50 bp mRNA linear EST 26-JUN-2002
DEFINITION rd08f05.y1 Meloidogyne incognita egg SL1 TOPO v1 Meloidogyne incognita cDNA 5', mRNA sequence.
ACCESSION BQ613522
VERSION BQ613522.1 GI:21603191
KEYWORDS EST.
SOURCE Meloidogyne incognita (southern root-knot nematode)
ORGANISM Meloidogyne incognita
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE 1 (bases 1 to 50)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Meloidogyne incognita eggs were provided by Andrew Kloek of Divergence Inc., St. Louis, MO.
Putative full length read
The vector to vector length is 65
Seq primer: -40RP from Gibco.

FEATURES
source Location/Qualifiers
1. .50
/organism="Meloidogyne incognita"
/mol_type="mRNA"
/db_xref="taxon:6306"
/dev_stage="egg"
/lab_host="DH10B (Invitrogen)"
/clone_lib="Meloidogyne incognita egg SL1 TOPO v1"
/note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI; Site_2: EcoRI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. Meloidogyne incognita eggs were provided by Andrew Kloek of Divergence Inc., St. Louis, MO."

ORIGIN

Query Match 40.6%; Score 13; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GTTTTGTCGTTTT 18
|||||||||||||
Db 15 GTTTTGTCGTTTT 3

RESULT 3
AJ600996/c
LOCUS AJ600996 23 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 518D07, genomic survey sequence.
ACCESSION AJ600996
VERSION AJ600996.1 GI:37950624
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 23)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

FEATURES
source Location/Qualifiers
1. .23
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="518D07"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .23
/note="T-DNA flanking sequence right border"

ORIGIN

Query Match 37.5%; Score 12; DB 9; Length 23;

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  Best Local Similarity   100.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTTTGTCGTTTT 18
              ||||||||||||
Db         15 TTTTGTCGTTTT 4


RESULT 4
AJ595925/c
LOCUS       AJ595925                 34 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            425H07, genomic survey sequence.
ACCESSION   AJ595925
VERSION     AJ595925.1  GI:37945553
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 34)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="425H07"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .34
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match           37.5%;  Score 12;  DB 9;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 TTTGTCGTTTTG 19
              ||||||||||||
Db         15 TTTGTCGTTTTG 4


RESULT 5
BH863768
LOCUS       BH863768                 47 bp    DNA     linear   GSS 05-AUG-2002
DEFINITION  SALK_094542 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_094542, genomic survey sequence.
ACCESSION   BH863768
VERSION     BH863768.1  GI:22099666
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 47)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within 300 bases of the 5' end of
            At5g37350.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .47
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_094542"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match           37.5%;  Score 12;  DB 8;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTGTC 13
              ||||||||||||
Db          3 CGTCGTTTTGTC 14


RESULT 6
AU256787/c
LOCUS       AU256787                 49 bp    mRNA    linear   EST 25-APR-2002
DEFINITION  AU256787 3'-directed mouse cDNA library Mus musculus cDNA clone
            BED0008976 3', mRNA sequence.
ACCESSION   AU256787
VERSION     AU256787.1  GI:20320777
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Kato,K. and Matoba,R.
  TITLE     Generation of expressed sequence tags from mouse brain
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kikuya Kato
            Graduate School of Biological Sciences
            Nara Institute of Science and Technology
            8916-5 Takayama, Ikoma, Nara 630-0101, Japan
            Tel: 81-743-72-5581
            Fax: 81-743-72-5589
```

Email: kkato@bs.aist-nara.ac.jp,
URL:http://love2.aist-nara.ac.jp/BED/index.html.
FEATURES Location/Qualifiers
source 1. .49
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0008976"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
ORIGIN

Query Match 37.5%; Score 12; DB 1; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TTTTGTCGTTTT 18
||||||||||||
Db 36 TTTTGTCGTTTT 25

RESULT 7
AZ472468
LOCUS AZ472468 50 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0287P08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0287P08 R, genomic survey sequence.
ACCESSION AZ472468
VERSION AZ472468.1 GI:10630593
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0287 row: P column: 08
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.
FEATURES Location/Qualifiers
source 1. .50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0287P08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 37.5%; Score 12; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TTGTCGTTTTGT 20
||||||||||||
Db 12 TTGTCGTTTTGT 23

RESULT 8
BX286679
LOCUS BX286679 56 bp DNA linear GSS 02-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-392H12-018271, genomic survey sequence.
ACCESSION BX286679
VERSION BX286679.1 GI:28885675
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
MEDLINE 23117147
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL BioTechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 56)
AUTHORS Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T20L15. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES Location/Qualifiers
source 1. .56
/organism="Arabidopsis thaliana"

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                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-392H12-018271"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Col-0"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161 (GenBank accession number: AJ537514). The
                     lines contain one or more T-DNA insertions. The DNA
                     fragment(s) resulting from the PCR were directly sequenced
                     to determine the genomic sequence flanking the insertion.
                     T-DNA derived sequences were removed."
ORIGIN

  Query Match             37.5%;  Score 12;  DB 9;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GTTTTGTCGTTT 17
              ||||||||||||
Db         42 GTTTTGTCGTTT 53


RESULT 9
AL754515
LOCUS       AL754515                 57 bp    DNA     linear   GSS 01-APR-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-054F09-012480,
            genomic survey sequence.
ACCESSION   AL754515
VERSION     AL754515.1  GI:21487013
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
  TITLE     GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
            the identification of T-DNA insertion mutants in Arabidopsis
            thaliana
  JOURNAL   Bioinformatics 19 (11), 1441-1442 (2003)
  MEDLINE   22755829
   PUBMED   12874060
REFERENCE   2
  AUTHORS   Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
            Weisshaar,B.
  TITLE     An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
            flanking sequence tag-based reverse genetics
  JOURNAL   Plant Mol. Biol. 53 (1-2), 247-259 (2003)
  MEDLINE   23117147
   PUBMED   14756321
REFERENCE   3
  AUTHORS   Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
            Weisshaar,B.
  TITLE     High-throughput generation of sequence indexes from T-DNA
            mutagenized Arabidopsis thaliana lines
  JOURNAL   BioTechniques 35 (6), 1164-1168 (2003)
   PUBMED   14682050
REFERENCE   4  (bases 1 to 57)
  AUTHORS   Rosso,M.G., Li,Y., Strizhov,N. and Weisshaar,B.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
            Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT     This sequence has been recovered from the left border of the T-DNA.
            It indicates an insertion within the locus defined by BAC clone
            f19i3. Details on the protocols used for generation of the sequence
            are described in References 1-3. The sequences are generated at the
            MPI for Plant Breeding Research in the context of the GABI-Kat
            project. GABI-Kat is part of the German Plant Genomics program
            designated 'GABI'. Information on line availability can be found
            at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-054F09-012480"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
                     /ecotype="Col-0"
                     /note="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161 (GenBank accession number: AJ537514). The
                     lines contain one or more T-DNA insertions. The DNA
                     fragment(s) resulting from the PCR were directly sequenced
                     to determine the genomic sequence flanking the insertion.
                     T-DNA derived sequences were removed."
ORIGIN

  Query Match             37.5%;  Score 12;  DB 9;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TTTTGTCGTTTT 18
              ||||||||||||
Db         46 TTTTGTCGTTTT 57


RESULT 10
AV964458/c
LOCUS       AV964458                 60 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV964458 Nori Satoh unpublished cDNA library, larva Ciona
            intestinalis cDNA clone cilv13e18 5', mRNA sequence.
ACCESSION   AV964458
VERSION     AV964458.1  GI:19454154
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cilv13e18"
                     /tissue_type="whole animal"
                     /dev_stage="larva"
                     /clone_lib="Nori Satoh unpublished cDNA library, larva"
ORIGIN

  Query Match             37.5%;  Score 12;  DB 2;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 GTTTTGTCGTTT 17
              ||||||||||||
Db         14 GTTTTGTCGTTT 3


RESULT 11
BH863639
LOCUS       BH863639                 62 bp    DNA     linear   GSS 05-AUG-2002
```

```
DEFINITION  SALK_094273 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_094273, genomic survey sequence.
ACCESSION   BH863639
VERSION     BH863639.1  GI:22099493
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 62)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within 300 bases of the 5' end of
            At5g37350.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .62
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_094273"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN
```

```
  Query Match             37.5%;  Score 12;  DB 8;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CGTCGTTTTGTC 13
              ||||||||||||
Db         18 CGTCGTTTTGTC 29
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```
RESULT 12
CB064048
LOCUS       CB064048                  63 bp    mRNA    linear   EST 21-JAN-2003
DEFINITION  py03c06.y1 Haemonchus contortus whole worm pAMP1 v1 Haemonchus
            contortus cDNA 5', mRNA sequence.
ACCESSION   CB064048
VERSION     CB064048.1  GI:27809626
KEYWORDS    EST.
SOURCE      Haemonchus contortus
  ORGANISM  Haemonchus contortus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
            Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
            Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
            Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
            Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
            Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Claire Murphy and Dr. James McCarter
            at Washington University, St. Louis. The cDNA was made by using
            Dynabead oligo-dT priming (Dynal). PCR based library using a
            modified protocol from the SMART PCR cDNA Synthesis Kit from
            Clontech. Directionally cloned into the UDG sites of pAMP1. Whole
            worm RNA was provided by Dr. Douglas Jasmer of Washington State
            University (djasmer@vetmed.wsu.edu).
            Seq primer: Primer name ambiguous.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Haemonchus contortus"
                     /mol_type="mRNA"
                     /db_xref="taxon:6289"
                     /tissue_type="whole organism"
                     /lab_host="DH10B"
                     /clone_lib="Haemonchus contortus whole worm pAMP1 v1"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI; The
                     library was constructed by Claire Murphy and Dr. James
                     McCarter at Washington University, St. Louis. The cDNA was
                     made by using Dynabead oligo-dT priming (Dynal). PCR based
                     library using a modified protocol from the SMART PCR cDNA
                     Synthesis Kit from Clontech. Directionally cloned into the
                     UDG sites of pAMP1. Whole worm RNA was provided by Dr.
                     Douglas Jasmer of Washington State University
                     (djasmer@vetmed.wsu.edu)."
ORIGIN
```

```
  Query Match             37.5%;  Score 12;  DB 6;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 4.6e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCGTCGTTTTGT 12
              ||||||||||||
Db         16 TCGTCGTTTTGT 27
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```
RESULT 13
CB192029
LOCUS       CB192029                  63 bp    mRNA    linear   EST 05-FEB-2003
DEFINITION  py23h12.y1 Haemonchus contortus whole worm pAMP1 v1 Haemonchus
            contortus cDNA 5', mRNA sequence.
ACCESSION   CB192029
VERSION     CB192029.1  GI:28255421
KEYWORDS    EST.
SOURCE      Haemonchus contortus
  ORGANISM  Haemonchus contortus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
            Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
            Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
            Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
            Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
            Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
  TITLE     The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
```

Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Whole worm RNA was provided by Dr. Douglas Jasmer of Washington State University (djasmer@vetmed.wsu.edu).
Seq primer: Primer name ambiguous.

FEATURES Location/Qualifiers
source 1. .63
/organism="Haemonchus contortus"
/mol_type="mRNA"
/db_xref="taxon:6289"
/tissue_type="whole organism"
/lab_host="DH10B"
/clone_lib="Haemonchus contortus whole worm pAMP1 v1"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Whole worm RNA was provided by Dr. Douglas Jasmer of Washington State University (djasmer@vetmed.wsu.edu)."

ORIGIN

Query Match 37.5%; Score 12; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGT 12
||||||||||||
Db 15 TCGTCGTTTTGT 26

RESULT 14
CB191498
LOCUS CB191498 64 bp mRNA linear EST 05-FEB-2003
DEFINITION py32h10.y1 Haemonchus contortus whole worm pAMP1 v1 Haemonchus contortus cDNA 5', mRNA sequence.
ACCESSION CB191498
VERSION CB191498.1 GI:28254890
KEYWORDS EST.
SOURCE Haemonchus contortus
ORGANISM Haemonchus contortus
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
REFERENCE 1 (bases 1 to 64)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Whole worm RNA was provided by Dr. Douglas Jasmer of Washington State University (djasmer@vetmed.wsu.edu).
Seq primer: Primer name ambiguous.

FEATURES Location/Qualifiers
source 1. .64
/organism="Haemonchus contortus"
/mol_type="mRNA"
/db_xref="taxon:6289"
/tissue_type="whole organism"
/lab_host="DH10B"
/clone_lib="Haemonchus contortus whole worm pAMP1 v1"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Whole worm RNA was provided by Dr. Douglas Jasmer of Washington State University (djasmer@vetmed.wsu.edu)."

ORIGIN

Query Match 37.5%; Score 12; DB 6; Length 64;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTGT 12
||||||||||||
Db 16 TCGTCGTTTTGT 27

RESULT 15
BH848405
LOCUS BH848405 23 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK_068149.48.55.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_068149.48.55.x, genomic survey sequence.
ACCESSION BH848405
VERSION BH848405.1 GI:21419276
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 23)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES Location/Qualifiers
source 1. .23
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_068149.48.55.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can

ORIGIN be found at http://signal.salk.edu/tdna_protocols.html"

Query Match 34.4%; Score 11; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGTTTTG 11
||||||||||||
Db 6 TCGTCGTTTTG 16

Search completed: February 14, 2005, 09:29:29
Job time : 7564 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 17:14:08 ; Search time 170 Seconds
(without alignments)
102.378 Million cell updates/sec

Title: US-10-076-674A-9
Perfect score: 243
Sequence: 1 TAKSKKFPSYTATYQFGGLS.....IVHRLEGVGGEHWSYGLRPG 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	243	100.0	45	2	AAR62721	Aar62721 LHRH-cont
2	243	100.0	45	7	ADD89949	Add89949 LHRH pept
3	243	100.0	45	8	ADJ56908	Adj56908 Human LHR
4	235	96.7	45	3	AAY68573	Aay68573 Peptide i
5	235	96.7	45	3	AAY91165	Aay91165 Modified
6	216.5	89.1	46	2	AAR62728	Aar62728 LHRH-cont
7	213	87.7	49	3	AAY91177	Aay91177 Modified
8	211	86.8	45	3	AAY68577	Aay68577 Peptide i
9	211	86.8	45	3	AAY91172	Aay91172 Modified
10	208	85.6	47	3	AAY68583	Aay68583 Peptide i
11	208	85.6	47	3	AAY91180	Aay91180 Inv epito
12	206	84.8	45	3	AAY91166	Aay91166 Modified
13	203	83.5	47	3	AAY68586	Aay68586 Peptide i
14	203	83.5	47	3	AAY91183	Aay91183 Inv epito
15	199	81.9	45	3	AAY68571	Aay68571 Peptide i
16	187	77.0	49	3	AAY68585	Aay68585 Peptide i
17	187	77.0	49	3	AAY91178	Aay91178 Modified
18	187	77.0	49	3	AAY91182	Aay91182 Inv epito
19	181	74.5	49	3	AAY68580	Aay68580 Peptide i
20	180	74.1	35	2	AAR65381	Aar65381 Universal
21	169.5	69.8	48	2	AAR62725	Aar62725 LHRH-cont
22	159	65.4	49	2	AAR62724	Aar62724 LHRH-cont
23	157	64.6	45	7	ADD89948	Add89948 LHRH pept
24	157	64.6	45	8	ADJ56907	Adj56907 Human LHR
25	156.5	64.4	54	2	AAR62722	Aar62722 LHRH-cont
26	156	64.2	45	2	AAR62720	Aar62720 LHRH-cont
27	152	62.6	47	2	AAR62723	Aar62723 LHRH-cont
28	151.5	62.3	46	3	AAY68595	Aay68595 Peptide i
29	151.5	62.3	46	3	AAY91195	Aay91195 Inv epito
30	150.5	61.9	48	2	AAR62729	Aar62729 LHRH-cont
31	150	61.7	42	2	AAR62708	Aar62708 LHRH-cont
32	150	61.7	80	3	AAY68530	Aay68530 Synthetic
33	147	60.5	27	2	AAR62707	Aar62707 LHRH-cont
34	147	60.5	27	3	AAY68567	Aay68567 Peptide i
35	147	60.5	27	3	AAY91156	Aay91156 MVF Th ep
36	144	59.3	27	3	AAY91163	Aay91163 Modified
37	139	57.2	27	3	AAY91161	Aay91161 Modified
38	139	57.2	27	3	AAY91167	Aay91167 Modified
39	137	56.4	28	3	AAY91158	Aay91158 Modified
40	134	55.1	27	3	AAY68575	Aay68575 Peptide i
41	134	55.1	27	3	AAY91170	Aay91170 Modified
42	133	54.7	31	3	AAY91175	Aay91175 Modified
43	131	53.9	28	2	AAR62726	Aar62726 LHRH-cont
44	130	53.5	28	3	AAY91159	Aay91159 Modified
45	130	53.5	31	3	AAY91179	Aay91179 Modified

ALIGNMENTS

RESULT 1
AAR62721
ID AAR62721 standard; peptide; 45 AA.
XX
AC AAR62721;
XX
DT 25-MAR-2003 (revised)
DT 10-SEP-1995 (first entry)
XX
DE LHRH-containing immunogenic peptide.
XX
KW Helper T cell epitope; universal immune stimulator; invasin; hapten;
KW vaccine; LHRH; luteinising hormone releasing hormone; prostate;
KW androgen-dependent carcinoma; antitumour; infertility;
KW measles virus F protein.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Domain 1. .16
FT /note= "invasin domain"
FT Domain 19. .33
FT /note= "measles virus F protein helper T cell epitope"
FT Domain 36. .45
FT /note= "LHRH hapten"
XX
PN WO9425060-A1
XX
PD 10-NOV-1994.
XX
PF 28-APR-1994; 94WO-US004832.
XX
PR 27-APR-1993; 93US-00057166.
PR 14-APR-1994; 94US-00229275.
XX
PA (LADD/) LADD A E.
PA (WANG/) WANG C Y.
PA (ZAMB/) ZAMB T.
XX
PI Ladd AE, Wang CY, Zamb T;
XX
DR WPI; 1994-357910/44.
XX
PT Immunogenic luteinising hormone releasing hormone peptide(s) - that
PT suppress LHRH activity in males and females.
XX
PS Claim 8; Page 88; 213pp; English.
XX

CC Synthetic immunogenic peptides are provided in which a universal immune
CC stimulator is linked to a peptide or protein hapten containing B cell
CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
CC potent immune responses to the coupled peptide or protein. The stimulator
CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
CC immune response to the coupled peptide in members of a heterogeneous
CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
CC sequence from the invasin protein of Yersinia. Spacer amino acid
CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
CC domains and between the immune stimulator and hapten components. When the
CC hapten is LHRH, then optionally the invasin domain can be omitted from
CC the immune stimulator component. The present sequence represents an LHRH-
CC containing immunogenic peptide as above which can be used as a potent
CC vaccine for treating e.g. prostatic hyperplasia, androgen-dependent
CC carcinoma, prostatic carcinoma, testicular carcinoma, endometriosis,
CC benign uterine tumours, recurrent functional ovarian cysts, (severe)
CC premenstrual syndrome or oestrogen-dependent breast cancer, or for
CC induction of infertility. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 45 AA;

```
  Query Match             100.0%;  Score 243;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-27;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
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RESULT 2
ADD89949
ID ADD89949 standard; protein; 45 AA.
XX
AC ADD89949;
XX
DT 29-JAN-2004 (first entry)
XX
DE LHRH peptide used in immunostimulant complex for prostate cancer vaccine.
XX
KW Immunostimulant; vaccine; human; immunogen; LHRH; immunotherapy;
KW prostate cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003068169-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004711.
XX
PR 14-FEB-2002; 2002US-00076674.
PR 31-JAN-2003; 2003US-00076674.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Sokoll KK;
XX
DR WPI; 2003-778890/73.
XX
PT Stabilized immunostimulating complex, useful for vaccination, e.g.
PT against human immune deficiency viruses, comprises cationic peptide
PT immunogen and anionic oligonucleotide.
XX
PS Claim 17; SEQ ID NO 9; 159pp; English.
XX
CC The present sequence is that of a synthetic immunogenic peptide derived
CC from human LHRH. This is an example of peptides that can be used in
CC claimed immunostimulatory complexes of the invention that are
CC specifically adapted to act as adjuvant and as peptide immunogen
CC stabiliser. The complexes comprise a CpG oligonucleotide and a
CC biologically active peptide immunogen. The complex is particulate and can
CC efficiently present peptide immunogens to the cells of the immune system
CC to produce an immune response. The complexes may be prepared with various
CC ratios of peptides to CpG oligonucleotides to provide different physical
CC properties, such as the size of the microparticle. An immunostimulatory
CC complex comprising the present LHRH derived peptide can be used in a
CC vaccine for prostate cancer.
XX
SQ Sequence 45 AA;

```
  Query Match             100.0%;  Score 243;  DB 7;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-27;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
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RESULT 3
ADJ56908
ID ADJ56908 standard; peptide; 45 AA.
XX
AC ADJ56908;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human LHRH immunogenic peptide #3.
XX
KW Immunostimulatory complex; adjuvant; peptide immunogen stabiliser;
KW water-in-oil emulsion; suspension; vaccine; prostate cancer;
KW hormone ablation; allergy; HIV infection; foot-and-mouth disease;
KW therapy; human; antigen; LHRH.
XX
OS Homo sapiens.
XX
PN US2004009897-A1.
XX
PD 15-JAN-2004.
XX
PF 21-MAY-2003; 2003US-00355161.
XX
PR 14-FEB-2002; 2002US-00076674.
XX
PA (SOKO/) SOKOLL K K.
XX
PI Sokoll KK;
XX
DR WPI; 2004-212745/20.
XX
PT Stabilized immunostimulatory complex useful for treating allergy, HIV
PT infection or prostate cancer, comprising cationic peptide immunogen and
PT anionic CpG oligonucleotide.
XX
PS Claim 17; SEQ ID NO 9; 63pp; English.
XX
CC The invention relates to an immunostimulatory complex specifically
CC adapted to act as adjuvant and as a peptide immunogen stabiliser. The
CC invention is useful for preparing a water-in-oil emulsion, suspension and
CC vaccine. It is also useful for treating prostate cancer, hormone
CC ablation, allergy, HIV infection, foot-and-mouth disease, etc. The
CC present sequence is human LHRH immunogenic peptide used in the invention.
XX
SQ Sequence 45 AA;

```
  Query Match             100.0%;  Score 243;  DB 8;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-27;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
```

```
RESULT 4
AAY68573
ID   AAY68573 standard; peptide; 45 AA.
XX
AC   AAY68573;
XX
DT   05-MAY-2000  (first entry)
XX
DE   Peptide immunogen comprising a Th epitope and LHRH target antigen.
XX
KW   Helper T cell epitope; F protein; Measles virus; peptide immunogen; LHRH;
KW   luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW   oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW   vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW   breast cancer; endometriosis; boar taint; meat quality; invasin domain;
KW   immunocastration.
XX
OS   Synthetic.
OS   Yersinia sp.
OS   Measles virus.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .16
FT                   /note= "invasin domain AAY68565"
FT   Peptide         17. .18
FT                   /note= "spacer"
FT   Peptide         19. .33
FT                   /note= "helper Th epitope AAY68544"
FT   Peptide         34. .35
FT                   /note= "spacer"
FT   Peptide         36. .45
FT                   /note= "LHRH antigenic epitope AAY68566"
XX
PN   WO9966952-A1.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013960.
XX
PR   20-JUN-1998;   98US-00100414.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160562/14.
XX
PT   New peptide immunogen containing luteinizing hormone-releasing hormone
PT   antigen site and helper T cell epitope, for e.g. contraception and
PT   treatment of cancer.
XX
PS   Claim 9; Page 71; 102pp; English.
XX
CC   The present sequence represents a peptide immunogen comprising an invasin
CC   domain immunostimulatory peptide of Yersinia sp., a synthetic helper T
CC   cell (Th) epitope and a target antigen, luteinising hormone-releasing
CC   hormone (LHRH). The synthetic Th epitope is derived from a structured
CC   synthetic antigen library (SSAL) designated SSAL1 Th1. SSAL Th1 is
CC   modelled after a promiscuous epitope taken from the F protein of the
CC   Measles virus. The peptide immunogens cause induction of a specific
CC   immune response to LHRH which is involved in regulation of
CC   spermatogenesis, ovulation, oestrus, sexual development and secretion of
CC   sex hormones. Provision of a promiscuous T helper epitope (which is
CC   functional in genetically diverse subjects) provides optimum
CC   immunogenicity to the B cell epitopes of the target antigen and thus high
CC   antibody titres against the target antigen. The peptide immunogens of the
CC   invention are used to vaccinate against mammalian LHRH, for use as
CC   (reversible) contraceptive; control of hormone-dependent tumours (cancer
CC   of prostate or breast, also endometriosis); to prevent boar taint (and
CC   improve meat quality) and for immunocastration
XX
SQ   Sequence 45 AA;

  Query Match             96.7%;  Score 235;  DB 3;  Length 45;
  Best Local Similarity   91.1%;  Pred. No. 5.7e-26;
  Matches   41;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||:||||||||::||:||||||||||||
Db          1 TAKSKKFPSYTATYQFGGISEIKGVIVHKIEGIGGEHWSYGLRPG 45


RESULT 5
AAY91165
ID   AAY91165 standard; peptide; 45 AA.
XX
AC   AAY91165;
XX
DT   12-SEP-2003  (revised)
DT   22-MAY-2000  (first entry)
XX
DE   Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:45.
XX
KW   Promiscuous T-cell epitope; measles virus F protein; MVF;
KW   hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW   luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW   somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW   foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW   Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW   cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS   Measles virus.
OS   Rattus sp.
OS   Chimeric.
XX
PN   WO9966957-A2.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013975.
XX
PR   20-JUN-1998;   98US-00100412.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160564/14.
XX
PT   New artificial T helper cell epitope and derived immunogens with target
PT   antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT   or human immune deficiency virus.
XX
PS   Example 1; Page 80; 129pp; English.
XX
CC   The invention relates to novel promiscuous T helper cell epitopes (Th),
CC   and immunogenic peptides comprising the Th epitopes of the invention
CC   along with B cell epitopes. The Th epitopes and peptide immunogens
CC   containing them, are used to induce a T helper cell response,
CC   specifically against Plasmodium falciparum, cholesteryl ester transport
CC   protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC   immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC   peptide immunogens may be used for prevention and/or treatment of
CC   infections (HIV, foot-and-mouth disease or malaria); for cancer
CC   immunotherapy; for inhibition of the action of luteinising hormone
CC   releasing hormone (LHRH) for contraception, treatment of hormone-
CC   dependent cancer, prevention of boar taint in meat, and immunocastration)
CC   ; for promoting the growth of animals; or for treating allergies or
CC   arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC   genetically diverse subjects) into an immunogen improves capacity to
CC   induce a strong T helper cell-mediated immune response, resulting in
CC   production of antibodies against a target antigen. Th can replace carrier
CC   proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC   represents a promiscuous T helper epitope from the measles virus F (MVF)
CC   protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
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CC   represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC   AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC   surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC   derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC   Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC   promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC   used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC   AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC   epitope. Somatostatin immunogens may be used to promote growth in
CC   livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC   AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC   be used to prevent HIV infection of T cells. AAY90212 is a modified
CC   version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC   are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC   treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC   disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC   peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC   circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC   antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC   AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC   immunogens comprising a CETP peptide and a Th epitope which may be used
CC   to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC   and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
CC   Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC   HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC   vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC   invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC   both of which may optionally be used in the antigenic peptides of the
CC   invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ   Sequence 45 AA;

  Query Match             96.7%;  Score 235;  DB 3;  Length 45;
  Best Local Similarity   91.1%;  Pred. No. 5.7e-26;
  Matches   41;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||:||||||||::||:||||||||||||
Db          1 TAKSKKFPSYTATYQFGGISEIKGVIVHKIEGIGGEHWSYGLRPG 45


RESULT 6
AAR62728
ID   AAR62728 standard; peptide; 46 AA.
XX
AC   AAR62728;
XX
DT   25-MAR-2003  (revised)
DT   17-SEP-1995  (first entry)
XX
DE   LHRH-containing immunogenic peptide.
XX
KW   Helper T cell epitope; universal immune stimulator; invasin; hapten;
KW   vaccine; LHRH; luteinising hormone releasing hormone; prostate;
KW   androgen-dependent carcinoma; antitumour; infertility;
KW   structured synthetic antigen library; SSAL.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Domain          1. .16
FT                   /note= "invasin domain"
FT   Domain          19. .34
FT                   /note= "structured synthetic antigen library (see US Ser.
FT                   No. 143312, 26 Oct 1993), where the variant positions
FT                   noted below may be a mixture of the specified residues.
FT                   This domain functions as a helper T cell epitope"
FT   Misc-difference 19
FT                   /label= Asp, Glu
FT   Misc-difference 20
FT                   /label= Leu, Ile, Val, Phe
FT   Misc-difference 22
FT                   /label= Glu, Asp
FT   Misc-difference 23
FT                   /label= Leu, Ile, Val, Phe
FT   Misc-difference 24
FT                   /label= Lys, Arg
FT   Misc-difference 26
FT                   /label= Leu, Ile, Val, Phe
FT   Misc-difference 27
FT                   /label= Leu, Ile, Val, Phe
FT   Misc-difference 28
FT                   /label= Leu, Ile, Val, Phe
FT   Misc-difference 30
FT                   /label= Lys, Arg
FT   Misc-difference 31
FT                   /label= Leu, Ile, Val, Phe
FT   Misc-difference 32
FT                   /label= Glu, Asp
FT   Misc-difference 34
FT                   /label= Leu, Ile, Val, Phe
FT   Domain          37. .46
FT                   /note= "LHRH hapten"
XX
PN   WO9425060-A1.
XX
PD   10-NOV-1994.
XX
PF   28-APR-1994;   94WO-US004832.
XX
PR   27-APR-1993;   93US-00057166.
PR   14-APR-1994;   94US-00229275.
XX
PA   (LADD/) LADD A E.
PA   (WANG/) WANG C Y.
PA   (ZAMB/) ZAMB T.
XX
PI   Ladd AE,  Wang CY,  Zamb T;
XX
DR   WPI; 1994-357910/44.
XX
PT   Immunogenic luteinising hormone releasing hormone peptide(s) - that
PT   suppress LHRH activity in males and females.
XX
PS   Claim 8; Page 88; 213pp; English.
XX
CC   Synthetic immunogenic peptides are provided in which a universal immune
CC   stimulator is linked to a peptide or protein hapten containing B cell
CC   and/or cytotoxic T lymphocyte epitopes, giving a product which causes
CC   potent immune responses to the coupled peptide or protein. The stimulator
CC   consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
CC   immune response to the coupled peptide in members of a heterogeneous
CC   population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
CC   sequence from the invasin protein of Yersinia. Spacer amino acid
CC   sequences (e.g. Gly-Gly) can be provided between the invasin and Th
CC   domains and between the immune stimulator and hapten components. When the
CC   hapten is LHRH, then optionally the invasin domain can be omitted from
CC   the immune stimulator component. The present sequence represents an LHRH-
CC   containing immunogenic peptide as above in which the Th is a structured
CC   synthetic antigen library (SSAL). The peptide can be used as a potent
CC   vaccine for treating e.g. prostatic hyperplasia, androgen-dependent
CC   carcinoma, prostatic carcinoma, testicular carcinoma, endometriosis,
CC   benign uterine tumours, recurrent functional ovarian cysts, (severe)
CC   premenstrual syndrome or oestrogen-dependent breast cancer, or for
CC   induction of infertility. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 46 AA;

  Query Match             89.1%;  Score 216.5;  DB 2;  Length 46;
  Best Local Similarity   84.8%;  Pred. No. 2.7e-23;
  Matches   39;  Conservative    6;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 TAKSKKFPSYTATYQFGG-LSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||| |||:||:::|:|||:|||||||||||
Db          1 TAKSKKFPSYTATYQFGGDLSELKGLLLHKLEGLGGEHWSYGLRPG 46
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RESULT 7
AAY91177
ID   AAY91177 standard; peptide; 49 AA.
XX
AC   AAY91177;
XX
DT   12-SEP-2003  (revised)
DT   22-MAY-2000  (first entry)
XX
DE   Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:57.
XX
KW   Promiscuous T-cell epitope; measles virus F protein; MVF;
KW   hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW   luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW   somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW   foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW   Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW   cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS   Measles virus.
OS   Rattus sp.
OS   Chimeric.
XX
PN   WO9966957-A2.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013975.
XX
PR   20-JUN-1998;   98US-00100412.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160564/14.
XX
PT   New artificial T helper cell epitope and derived immunogens with target
PT   antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT   or human immune deficiency virus.
XX
PS   Example 1; Page 85; 129pp; English.
XX
CC   The invention relates to novel promiscuous T helper cell epitopes (Th),
CC   and immunogenic peptides comprising the Th epitopes of the invention
CC   along with B cell epitopes. The Th epitopes and peptide immunogens
CC   containing them, are used to induce a T helper cell response,
CC   specifically against Plasmodium falciparum, cholesteryl ester transport
CC   protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC   immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC   peptide immunogens may be used for prevention and/or treatment of
CC   infections (HIV, foot-and-mouth disease or malaria); for cancer
CC   immunotherapy; for inhibition of the action of luteinising hormone
CC   releasing hormone (LHRH) for contraception, treatment of hormone-
CC   dependent cancer, prevention of boar taint in meat, and immunocastration)
CC   ; for promoting the growth of animals; or for treating allergies or
CC   arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC   genetically diverse subjects) into an immunogen improves capacity to
CC   induce a strong T helper cell-mediated immune response, resulting in
CC   production of antibodies against a target antigen. Th can replace carrier
CC   proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC   represents a promiscuous T helper epitope from the measles virus F (MVF)
CC   protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC   represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC   AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC   surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC   derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC   Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC   promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC   used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC   AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC   epitope. Somatostatin immunogens may be used to promote growth in
CC   livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC   AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC   be used to prevent HIV infection of T cells. AAY90212 is a modified
CC   version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC   are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC   treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC   disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC   peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC   circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC   antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC   AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC   immunogens comprising a CETP peptide and a Th epitope which may be used
CC   to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC   and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
CC   Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC   HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC   vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC   invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC   both of which may optionally be used in the antigenic peptides of the
CC   invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ   Sequence 49 AA;

  Query Match             87.7%;  Score 213;  DB 3;  Length 49;
  Best Local Similarity   83.7%;  Pred. No. 9.2e-23;
  Matches   41;  Conservative    4;  Mismatches    0;  Indels    4;  Gaps    2;

Qy          1 TAKSKKFPSYTATYQFGG--LSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
              |||||||||||||||||  :|||||||||::||:  ||||||||||||
Db          1 TAKSKKFPSYTATYQFGGISISEIKGVIVHKIEGILFGGEHWSYGLRPG 49


RESULT 8
AAY68577
ID   AAY68577 standard; peptide; 45 AA.
XX
AC   AAY68577;
XX
DT   05-MAY-2000  (first entry)
XX
DE   Peptide immunogen comprising a Th epitope and LHRH target antigen.
XX
KW   Helper T cell epitope; F protein; Measles virus; peptide immunogen; LHRH;
KW   luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW   oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW   vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW   breast cancer; endometriosis; boar taint; meat quality; invasin domain;
KW   immunocastration.
XX
OS   Synthetic.
OS   Yersinia sp.
OS   Measles virus.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .16
FT                   /note= "invasin domain AAY68565"
FT   Peptide         17. .18
FT                   /note= "spacer"
FT   Peptide         19. .33
FT                   /note= "helper Th epitope AAY68547"
FT   Peptide         34. .35
FT                   /note= "spacer"
FT   Peptide         36. .45
FT                   /note= "LHRH antigenic epitope AAY68566"
XX
PN   WO9966952-A1.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013960.
XX
PR   20-JUN-1998;   98US-00100414.
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XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160562/14.
XX
PT New peptide immunogen containing luteinizing hormone-releasing hormone
PT antigen site and helper T cell epitope, for e.g. contraception and
PT treatment of cancer.
XX
PS Claim 9; Page 73; 102pp; English.
XX
CC The present sequence represents a peptide immunogen comprising an invasin
CC domain immunostimulatory peptide of Yersinia sp., a synthetic helper T
CC cell (Th) epitope and a target antigen, luteinising hormone-releasing
CC hormone (LHRH). The synthetic Th epitope is derived from a structured
CC synthetic antigen library (SSAL) designated SSAL1 Th1. SSAL Th1 is
CC modelled after a promiscuous epitope taken from the F protein of the
CC Measles virus. The peptide immunogens cause induction of a specific
CC immune response to LHRH which is involved in regulation of
CC spermatogenesis, ovulation, oestrus, sexual development and secretion of
CC sex hormones. Provision of a promiscuous T helper epitope (which is
CC functional in genetically diverse subjects) provides optimum
CC immunogenicity to the B cell epitopes of the target antigen and thus high
CC antibody titres against the target antigen. The peptide immunogens of the
CC invention are used to vaccinate against mammalian LHRH, for use as
CC (reversible) contraceptive; control of hormone-dependent tumours (cancer
CC of prostate or breast, also endometriosis); to prevent boar taint (and
CC improve meat quality) and for immunocastration
XX
SQ Sequence 45 AA;

Query Match 86.8%; Score 211; DB 3; Length 45;
Best Local Similarity 88.9%; Pred. No. 1.6e-22;
Matches 40; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
||||||||||||||||||:||: ||| ||| ||||||||||||
Db 1 TAKSKKFPSYTATYQFGGLTEIRTVIVTRLETVGGEHWSYGLRPG 45

RESULT 9
AAY91172
ID AAY91172 standard; peptide; 45 AA.
XX
AC AAY91172;
XX
DT 12-SEP-2003 (revised)
DT 22-MAY-2000 (first entry)
XX
DE Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:52.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Measles virus.
OS Rattus sp.
OS Chimeric.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013975.
XX
PR 20-JUN-1998; 98US-00100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus.
XX
PS Example 1; Page 83; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and immunocastration)
CC ; for promoting the growth of animals; or for treating allergies or
CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC genetically diverse subjects) into an immunogen improves capacity to
CC induce a strong T helper cell-mediated immune response, resulting in
CC production of antibodies against a target antigen. Th can replace carrier
CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC represents a promiscuous T helper epitope from the measles virus F (MVF)
CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC epitope. Somatostatin immunogens may be used to promote growth in
CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC be used to prevent HIV infection of T cells. AAY90212 is a modified
CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC immunogens comprising a CETP peptide and a Th epitope which may be used
CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC both of which may optionally be used in the antigenic peptides of the
CC invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 45 AA;

Query Match 86.8%; Score 211; DB 3; Length 45;
Best Local Similarity 88.9%; Pred. No. 1.6e-22;
Matches 40; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
||||||||||||||||||:||: ||| ||| ||||||||||||
Db 1 TAKSKKFPSYTATYQFGGLTEIRTVIVTRLETVGGEHWSYGLRPG 45

```
RESULT 10
AAY68583
ID   AAY68583 standard; peptide; 47 AA.
XX
AC   AAY68583;
XX
DT   05-MAY-2000  (first entry)
XX
DE   Peptide immunogen comprising a Th epitope and LHRH target antigen.
XX
KW   Helper T cell epitope; F protein; Measles virus; peptide immunogen; LHRH;
KW   luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW   oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW   vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW   breast cancer; endometriosis; boar taint; meat quality; invasin domain;
KW   immunocastration.
XX
OS   Synthetic.
OS   Yersinia sp.
OS   Measles virus.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .16
FT                   /note= "invasin domain AAY68565"
FT   Peptide         17. .35
FT                   /note= "helper Th epitope AAY68551"
FT   Peptide         36. .37
FT                   /note= "spacer"
FT   Peptide         38. .47
FT                   /note= "LHRH antigenic epitope AAY68566"
XX
PN   WO9966952-A1.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013960.
XX
PR   20-JUN-1998;   98US-00100414.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160562/14.
XX
PT   New peptide immunogen containing luteinizing hormone-releasing hormone
PT   antigen site and helper T cell epitope, for e.g. contraception and
PT   treatment of cancer.
XX
PS   Claim 9; Page 80; 102pp; English.
XX
CC   The present sequence represents a peptide immunogen comprising an invasin
CC   domain immunostimulatory peptide of Yersinia sp., a synthetic helper T
CC   cell (Th) epitope and a target antigen, luteinising hormone-releasing
CC   hormone (LHRH). The synthetic Th epitope is derived from a structured
CC   synthetic antigen library (SSAL) designated SSAL1 Th1. SSAL Th1 is
CC   modelled after a promiscuous epitope taken from the F protein of the
CC   Measles virus. The peptide immunogens cause induction of a specific
CC   immune response to LHRH which is involved in regulation of
CC   spermatogenesis, ovulation, oestrus, sexual development and secretion of
CC   sex hormones. Provision of a promiscuous T helper epitope (which is
CC   functional in genetically diverse subjects) provides optimum
CC   immunogenicity to the B cell epitopes of the target antigen and thus high
CC   antibody titres against the target antigen. The peptide immunogens of the
CC   invention are used to vaccinate against mammalian LHRH, for use as
CC   (reversible) contraceptive; control of hormone-dependent tumours (cancer
CC   of prostate or breast, also endometriosis); to prevent boar taint (and
CC   improve meat quality) and for immunocastration
XX
SQ   Sequence 47 AA;

  Query Match             85.6%;  Score 208;  DB 3;  Length 47;
  Best Local Similarity   83.0%;  Pred. No. 4.6e-22;
  Matches   39;  Conservative    4;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
              ||||||||||||||||  :|||||||||::||:  ||||||||||||
Db          1 TAKSKKFPSYTATYQFISISEIKGVIVHKIEGILFGGEHWSYGLRPG 47


RESULT 11
AAY91180
ID   AAY91180 standard; peptide; 47 AA.
XX
AC   AAY91180;
XX
DT   12-SEP-2003  (revised)
DT   22-MAY-2000  (first entry)
XX
DE   Inv epitope/modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:60.
XX
KW   Promiscuous T-cell epitope; measles virus F protein; MVF;
KW   hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW   luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW   somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW   foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW   Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW   cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS   Measles virus.
OS   Rattus sp.
OS   Yersinia sp.
OS   Chimeric.
XX
PN   WO9966957-A2.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013975.
XX
PR   20-JUN-1998;   98US-00100412.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160564/14.
XX
PT   New artificial T helper cell epitope and derived immunogens with target
PT   antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT   or human immune deficiency virus.
XX
PS   Example 1; Page 86; 129pp; English.
XX
CC   The invention relates to novel promiscuous T helper cell epitopes (Th),
CC   and immunogenic peptides comprising the Th epitopes of the invention
CC   along with B cell epitopes. The Th epitopes and peptide immunogens
CC   containing them, are used to induce a T helper cell response,
CC   specifically against Plasmodium falciparum, cholesteryl ester transport
CC   protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC   immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC   peptide immunogens may be used for prevention and/or treatment of
CC   infections (HIV, foot-and-mouth disease or malaria); for cancer
CC   immunotherapy; for inhibition of the action of luteinising hormone
CC   releasing hormone (LHRH) for contraception, treatment of hormone-
CC   dependent cancer, prevention of boar taint in meat, and immunocastration)
CC   ; for promoting the growth of animals; or for treating allergies or
CC   arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC   genetically diverse subjects) into an immunogen improves capacity to
CC   induce a strong T helper cell-mediated immune response, resulting in
CC   production of antibodies against a target antigen. Th can replace carrier
CC   proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC   represents a promiscuous T helper epitope from the measles virus F (MVF)
CC   protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC   represent synthetic Th epitopes based on the MVF Th epitope. Sequence
```

CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV) surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-Y91244 are antigenic peptides comprising an LHRH sequence joined to a promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide used in these LHRH antigenic peptides. AAY91200 is somatostatin, and AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th epitope. Somatostatin immunogens may be used to promote growth in livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may be used to prevent HIV infection of T cells. AAY90212 is a modified version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219 are Th epitope/IgE CH3 antigenic peptides which may be used in the treatment of allergies. AAY91220 is a peptide derived from foot and mouth disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this peptide and a Th epitope. AAY91223 is a Plasmodium falciparum circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS antigen and an MVF Th epitope and may be used in a malaria vaccine. AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a CETP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 47 AA;

Query Match 85.6%; Score 208; DB 3; Length 47;
Best Local Similarity 83.0%; Pred. No. 4.6e-22;
Matches 39; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

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Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
              |||||||||||||||  :|||||||||::||:  ||||||||||||
Db          1 TAKSKKFPSYTATYQFISISEIKGVIVHKIEGILFGGEHWSYGLRPG 47
```

RESULT 12
AAY91166
ID AAY91166 standard; peptide; 45 AA.
XX
AC AAY91166;
XX
DT 12-SEP-2003 (revised)
DT 22-MAY-2000 (first entry)
XX
DE Modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:46.
XX
KW Promiscuous T-cell epitope; measles virus F protein; MVF;
KW hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS Measles virus.
OS Rattus sp.
OS Chimeric.
XX
PN WO9966957-A2.
XX
PD 29-DEC-1999.
XX
PF 21-JUN-1999; 99WO-US013975.
XX
PR 20-JUN-1998; 98US-00100412.
XX
PA (UNBI-) UNITED BIOMEDICAL INC.
XX
PI Wang CY;
XX
DR WPI; 2000-160564/14.
XX
PT New artificial T helper cell epitope and derived immunogens with target
PT antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT or human immune deficiency virus.
XX
PS Example 1; Page 81; 129pp; English.
XX
CC The invention relates to novel promiscuous T helper cell epitopes (Th),
CC and immunogenic peptides comprising the Th epitopes of the invention
CC along with B cell epitopes. The Th epitopes and peptide immunogens
CC containing them, are used to induce a T helper cell response,
CC specifically against Plasmodium falciparum, cholesteryl ester transport
CC protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC peptide immunogens may be used for prevention and/or treatment of
CC infections (HIV, foot-and-mouth disease or malaria); for cancer
CC immunotherapy; for inhibition of the action of luteinising hormone
CC releasing hormone (LHRH) for contraception, treatment of hormone-
CC dependent cancer, prevention of boar taint in meat, and immunocastration)
CC ; for promoting the growth of animals; or for treating allergies or
CC arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC genetically diverse subjects) into an immunogen improves capacity to
CC induce a strong T helper cell-mediated immune response, resulting in
CC production of antibodies against a target antigen. Th can replace carrier
CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC represents a promiscuous T helper epitope from the measles virus F (MVF)
CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC epitope. Somatostatin immunogens may be used to promote growth in
CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC be used to prevent HIV infection of T cells. AAY90212 is a modified
CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC immunogens comprising a CETP peptide and a Th epitope which may be used
CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC both of which may optionally be used in the antigenic peptides of the
CC invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 45 AA;

Query Match 84.8%; Score 206; DB 3; Length 45;
Best Local Similarity 82.2%; Pred. No. 8.4e-22;
Matches 37; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

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Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||||::||: ||| |:| :||||||||||||
Db          1 TAKSKKFPSYTATYQFGGITEIRTVIVTRIETIGGEHWSYGLRPG 45
```

RESULT 13
AAY68586

```
ID   AAY68586 standard; peptide; 47 AA.
XX
AC   AAY68586;
XX
DT   05-MAY-2000  (first entry)
XX
DE   Peptide immunogen comprising a Th epitope and LHRH target antigen.
XX
KW   Helper T cell epitope; F protein; Measles virus; peptide immunogen; LHRH;
KW   luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW   oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW   vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW   breast cancer; endometriosis; boar taint; meat quality; invasin domain;
KW   immunocastration.
XX
OS   Synthetic.
OS   Yersinia sp.
OS   Measles virus.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .16
FT                   /note= "invasin domain AAY68565"
FT   Peptide         17. .35
FT                   /note= "helper Th epitope AAY68553"
FT   Peptide         36. .37
FT                   /note= "spacer"
FT   Peptide         38. .47
FT                   /note= "LHRH antigenic epitope AAY68566"
XX
PN   WO9966952-A1.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013960.
XX
PR   20-JUN-1998;   98US-00100414.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160562/14.
XX
PT   New peptide immunogen containing luteinizing hormone-releasing hormone
PT   antigen site and helper T cell epitope, for e.g. contraception and
PT   treatment of cancer.
XX
PS   Claim 9; Page 81; 102pp; English.
XX
CC   The present sequence represents a peptide immunogen comprising an invasin
CC   domain immunostimulatory peptide of Yersinia sp., a synthetic helper T
CC   cell (Th) epitope and a target antigen, luteinising hormone-releasing
CC   hormone (LHRH). The synthetic Th epitope is derived from a structured
CC   synthetic antigen library (SSAL) designated SSAL1 Th1. SSAL Th1 is
CC   modelled after a promiscuous epitope taken from the F protein of the
CC   Measles virus. The peptide immunogens cause induction of a specific
CC   immune response to LHRH which is involved in regulation of
CC   spermatogenesis, ovulation, oestrus, sexual development and secretion of
CC   sex hormones. Provision of a promiscuous T helper epitope (which is
CC   functional in genetically diverse subjects) provides optimum
CC   immunogenicity to the B cell epitopes of the target antigen and thus high
CC   antibody titres against the target antigen. The peptide immunogens of the
CC   invention are used to vaccinate against mammalian LHRH, for use as
CC   (reversible) contraceptive; control of hormone-dependent tumours (cancer
CC   of prostate or breast, also endometriosis); to prevent boar taint (and
CC   improve meat quality) and for immunocastration
XX
SQ   Sequence 47 AA;

  Query Match             83.5%;  Score 203;  DB 3;  Length 47;
  Best Local Similarity   80.9%;  Pred. No. 2.4e-21;
  Matches   38;  Conservative    5;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
              ||||||||||||||||  :||:|||||::||:  ||||||||||||
Db          1 TAKSKKFPSYTATYQFISMSEMKGVIVHKMEGMLFGGEHWSYGLRPG 47

RESULT 14
AAY91183
ID   AAY91183 standard; peptide; 47 AA.
XX
AC   AAY91183;
XX
DT   12-SEP-2003  (revised)
DT   22-MAY-2000  (first entry)
XX
DE   Inv epitope/modified MVF Th epitope/LHRH antigenic peptide, SEQ ID NO:63.
XX
KW   Promiscuous T-cell epitope; measles virus F protein; MVF;
KW   hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope;
KW   luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;
KW   somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;
KW   foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic;
KW   Plasmodium falciparum; circumsporozoite; antimalarial; CETP;
KW   cholesteryl ester transport protein; anti-arteriosclerotic.
XX
OS   Measles virus.
OS   Rattus sp.
OS   Yersinia sp.
OS   Chimeric.
XX
PN   WO9966957-A2.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013975.
XX
PR   20-JUN-1998;   98US-00100412.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160564/14.
XX
PT   New artificial T helper cell epitope and derived immunogens with target
PT   antigenic site, for immunization against e.g. malaria, arteriosclerosis
PT   or human immune deficiency virus.
XX
PS   Example 1; Page 87; 129pp; English.
XX
CC   The invention relates to novel promiscuous T helper cell epitopes (Th),
CC   and immunogenic peptides comprising the Th epitopes of the invention
CC   along with B cell epitopes. The Th epitopes and peptide immunogens
CC   containing them, are used to induce a T helper cell response,
CC   specifically against Plasmodium falciparum, cholesteryl ester transport
CC   protein (CETP) or HIV epitopes, but more generally against any pathogen,
CC   immunoreactive self-antigen or tumour antigen. The Th epitopes and
CC   peptide immunogens may be used for prevention and/or treatment of
CC   infections (HIV, foot-and-mouth disease or malaria); for cancer
CC   immunotherapy; for inhibition of the action of luteinising hormone
CC   releasing hormone (LHRH) for contraception, treatment of hormone-
CC   dependent cancer, prevention of boar taint in meat, and immunocastration)
CC   ; for promoting the growth of animals; or for treating allergies or
CC   arteriosclerosis. Incorporation of a promiscuous Th (functional in
CC   genetically diverse subjects) into an immunogen improves capacity to
CC   induce a strong T helper cell-mediated immune response, resulting in
CC   production of antibodies against a target antigen. Th can replace carrier
CC   proteins and pathogen-derived T helper epitopes. Sequence AAY91121
CC   represents a promiscuous T helper epitope from the measles virus F (MVF)
CC   protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246
CC   represent synthetic Th epitopes based on the MVF Th epitope. Sequence
CC   AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)
CC   surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes
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CC   derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-
CC   Y91244 are antigenic peptides comprising an LHRH sequence joined to a
CC   promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide
CC   used in these LHRH antigenic peptides. AAY91200 is somatostatin, and
CC   AAY91201-Y91207 are antigenic peptides comprising somatostatin and a Th
CC   epitope. Somatostatin immunogens may be used to promote growth in
CC   livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and
CC   AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may
CC   be used to prevent HIV infection of T cells. AAY90212 is a modified
CC   version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219
CC   are Th epitope/IgE CH3 antigenic peptides which may be used in the
CC   treatment of allergies. AAY91220 is a peptide derived from foot and mouth
CC   disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this
CC   peptide and a Th epitope. AAY91223 is a Plasmodium falciparum
CC   circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS
CC   antigen and an MVF Th epitope and may be used in a malaria vaccine.
CC   AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are
CC   immunogens comprising a CETP peptide and a Th epitope which may be used
CC   to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247
CC   and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-
CC   Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and
CC   HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1
CC   vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
CC   invasin protein epitope from Yersinia species, and hinge spacer peptide,
CC   both of which may optionally be used in the antigenic peptides of the
CC   invention. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ   Sequence 47 AA;

  Query Match             83.5%;  Score 203;  DB 3;  Length 47;
  Best Local Similarity   80.9%;  Pred. No. 2.4e-21;
  Matches   38;  Conservative    5;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
              |||||||||||||||  :||:|||||::||:  ||||||||||||
Db          1 TAKSKKFPSYTATYQFISMSEMKGVIVHKMEGMLFGGEHWSYGLRPG 47


RESULT 15
AAY68571
ID   AAY68571 standard; peptide; 45 AA.
XX
AC   AAY68571;
XX
DT   05-MAY-2000  (first entry)
XX
DE   Peptide immunogen comprising a Th epitope and LHRH target antigen.
XX
KW   Helper T cell epitope; F protein; Measles virus; peptide immunogen; LHRH;
KW   luteinising hormone-releasing hormone; spermatogenesis; ovulation;
KW   oestrus; sexual development; sex hormone; promiscuous T helper epitope;
KW   vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
KW   breast cancer; endometriosis; boar taint; meat quality; invasin domain;
KW   immunocastration.
XX
OS   Synthetic.
OS   Yersinia sp.
OS   Measles virus.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .16
FT                   /note= "invasin domain AAY68565"
FT   Peptide         17. .18
FT                   /note= "spacer"
FT   Peptide         19. .33
FT                   /note= "helper Th epitope AAY68542"
FT   Misc-difference 20
FT                   /label= Ser, Thr
FT   Misc-difference 23
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FT   Peptide         34. .35
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FT                   /note= "LHRH antigenic epitope AAY68566"
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PN   WO9966952-A1.
XX
PD   29-DEC-1999.
XX
PF   21-JUN-1999;   99WO-US013960.
XX
PR   20-JUN-1998;   98US-00100414.
XX
PA   (UNBI-) UNITED BIOMEDICAL INC.
XX
PI   Wang CY;
XX
DR   WPI; 2000-160562/14.
XX
PT   New peptide immunogen containing luteinizing hormone-releasing hormone
PT   antigen site and helper T cell epitope, for e.g. contraception and
PT   treatment of cancer.
XX
PS   Claim 9; Page 69; 102pp; English.
XX
CC   The present sequence represents a peptide immunogen comprising an invasin
CC   domain immunostimulatory peptide of Yersinia sp., a synthetic helper T
CC   cell (Th) epitope and a target antigen, luteinising hormone-releasing
CC   hormone (LHRH). The synthetic Th epitope is derived from a structured
CC   synthetic antigen library (SSAL) designated SSAL1 Th1. SSAL Th1 is
CC   modelled after a promiscuous epitope taken from the F protein of the
CC   Measles virus. The peptide immunogens cause induction of a specific
CC   immune response to LHRH which is involved in regulation of
CC   spermatogenesis, ovulation, oestrus, sexual development and secretion of
CC   sex hormones. Provision of a promiscuous T helper epitope (which is
CC   functional in genetically diverse subjects) provides optimum
CC   immunogenicity to the B cell epitopes of the target antigen and thus high
CC   antibody titres against the target antigen. The peptide immunogens of the
CC   invention are used to vaccinate against mammalian LHRH, for use as
CC   (reversible) contraceptive; control of hormone-dependent tumours (cancer
CC   of prostate or breast, also endometriosis); to prevent boar taint (and
CC   improve meat quality) and for immunocastration
XX
SQ   Sequence 45 AA;

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  Best Local Similarity   80.0%;  Pred. No. 8.5e-21;
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Job time : 170 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 17:25:08 ; Search time 43 Seconds
(without alignments)
78.121 Million cell updates/sec

Title: US-10-076-674A-9
Perfect score: 243
Sequence: 1 TAKSKKFPSYTATYQFGGLS.....IVHRLEGVGGEHWSYGLRPG 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	243	100.0	45	1	US-08-446-692-33	Sequence 33, Appl
2	243	100.0	45	2	US-08-488-351A-33	Sequence 33, Appl
3	235	96.7	45	3	US-09-100-414B-45	Sequence 45, Appl
4	235	96.7	45	3	US-09-303-323-45	Sequence 45, Appl
5	235	96.7	45	4	US-09-770-014-45	Sequence 45, Appl
6	235	96.7	45	4	US-09-701-588C-45	Sequence 45, Appl
7	216.5	89.1	46	1	US-08-446-692-40	Sequence 40, Appl
8	216.5	89.1	46	2	US-08-488-351A-40	Sequence 40, Appl
9	213	87.7	49	3	US-09-100-414B-57	Sequence 57, Appl
10	213	87.7	49	3	US-09-303-323-57	Sequence 57, Appl
11	213	87.7	49	4	US-09-770-014-57	Sequence 57, Appl
12	213	87.7	49	4	US-09-701-588C-57	Sequence 57, Appl
13	211	86.8	45	3	US-09-100-414B-52	Sequence 52, Appl
14	211	86.8	45	3	US-09-303-323-52	Sequence 52, Appl
15	211	86.8	45	4	US-09-770-014-52	Sequence 52, Appl
16	211	86.8	45	4	US-09-701-588C-52	Sequence 52, Appl
17	208	85.6	47	3	US-09-100-414B-60	Sequence 60, Appl
18	208	85.6	47	3	US-09-303-323-60	Sequence 60, Appl
19	208	85.6	47	4	US-09-770-014-60	Sequence 60, Appl
20	208	85.6	47	4	US-09-701-588C-60	Sequence 60, Appl
21	206	84.8	45	3	US-09-100-414B-46	Sequence 46, Appl
22	206	84.8	45	3	US-09-303-323-46	Sequence 46, Appl
23	206	84.8	45	4	US-09-770-014-46	Sequence 46, Appl
24	206	84.8	45	4	US-09-701-588C-46	Sequence 46, Appl
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37	180	74.1	35	1	US-08-446-692-55	Sequence 55, Appl
38	180	74.1	35	2	US-08-488-351A-55	Sequence 55, Appl
39	169.5	69.8	48	1	US-08-446-692-37	Sequence 37, Appl
40	169.5	69.8	48	2	US-08-488-351A-37	Sequence 37, Appl
41	159	65.4	49	1	US-08-446-692-36	Sequence 36, Appl
42	159	65.4	49	2	US-08-488-351A-36	Sequence 36, Appl
43	156.5	64.4	54	1	US-08-446-692-34	Sequence 34, Appl
44	156.5	64.4	54	2	US-08-488-351A-34	Sequence 34, Appl
45	156	64.2	45	1	US-08-446-692-32	Sequence 32, Appl

ALIGNMENTS

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RESULT 1
US-08-446-692-33
; Sequence 33, Application US/08446692
; Patent No. 5759551
;  GENERAL INFORMATION:
;    APPLICANT:  Ladd, Anna
;    APPLICANT:  Wang, Chang Yi
;    APPLICANT:  Zamb, Timothy
;    TITLE OF INVENTION:  Immunogenic LHRH peptide constructs
;    TITLE OF INVENTION:  and synthetic universal immune stimulators for vaccines
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maria C.H. Lin
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10154-0053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,692
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria C.H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4146 US2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)415-8745
;      TELEFAX:  (516)751-6849
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-446-692-33

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Db          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
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RESULT 2
US-08-488-351A-33
; Sequence 33, Application US/08488351A
; Patent No. 5843446
;  GENERAL INFORMATION:
;     APPLICANT:  Ladd, Anna
;     APPLICANT:  Wang, Chang Yi
;     APPLICANT:  Zamb, Timothy
;     TITLE OF INVENTION:  Immunogenic LHRH peptide constructs
;     TITLE OF INVENTION:  and synthetic universal immune stimulators for vaccines
;     NUMBER OF SEQUENCES:  114
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Maria C.H. Lin
;       STREET:  345 Park Avenue
;       CITY:  New York
;       STATE:  NY
;       COUNTRY:  US
;       ZIP:  10154-0053
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/488,351A
;       FILING DATE:  7-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/446,692
;       FILING DATE:  7-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/229,275
;       FILING DATE:  14-APR-1994
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/057,166
;       FILING DATE:  27-APR-1992
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Maria C.H. Lin
;       REGISTRATION NUMBER:  29,323
;       REFERENCE/DOCKET NUMBER:  1151-4146 US2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212)415-8745
;       TELEFAX:  (516)751-6849
;  INFORMATION FOR SEQ ID NO:  33:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-488-351A-33

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Db          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45


RESULT 3
US-09-100-414B-45
; Sequence 45, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;     APPLICANT:  Wang, Chang Yi
;     TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;     TITLE OF INVENTION:  IMMUNOGENS
;     NUMBER OF SEQUENCES:  106
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Morgan & Finnegan, L.L.P.
;       STREET:  345 Park Avenue
;       CITY:  New York
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10154-0054
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
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;       OPERATING SYSTEM:  PC Windows
;       SOFTWARE:  Word 97
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;       APPLICATION NUMBER:  US/09/100,414B
;       FILING DATE:  20-JUNE-1998
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Maria H. Lin
;       REGISTRATION NUMBER:  29,323
;       REFERENCE/DOCKET NUMBER:  1151-4157
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-758-4800
;       TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  45:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-100-414B-45

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Db          1 TAKSKKFPSYTATYQFGGISEIKGVIVHKIEGIGGEHWSYGLRPG 45


RESULT 4
US-09-303-323-45
; Sequence 45, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;     APPLICANT:  Wang, Chang Yi
;     TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;     TITLE OF INVENTION:  IMMUNOGENS
;     NUMBER OF SEQUENCES:  106
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Morgan & Finnegan, L.L.P.
;       STREET:  345 Park Avenue
;       CITY:  New York
;       STATE:  NY
;       COUNTRY:  USA
;       ZIP:  10154-0054
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC Windows
;       SOFTWARE:  Word 97
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;       FILING DATE:  30-APR-1999
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  09/100,414
;       FILING DATE:  20-JUNE-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Maria H. Lin
;       REGISTRATION NUMBER:  29,323
;       REFERENCE/DOCKET NUMBER:  1151-4157
;     TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  212-758-4800
;       TELEFAX:  212-751-6849
;   INFORMATION FOR SEQ ID NO:  45:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  45 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-303-323-45

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RESULT 5
US-09-770-014-45
; Sequence 45, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC compatible
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;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
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;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  45:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-45

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  Matches   41;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 TAKSKKFPSYTATYQFGGISEIKGVIVHKIEGIGGEHWSYGLRPG 45


RESULT 6
US-09-701-588C-45
; Sequence 45, Application US/09701588C
; Patent No. 6713301
;  GENERAL INFORMATION:
;       APPLICANT: UNITED BIOMEDICAL INC., ET AL.
;       TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
;                           EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
;                           EPTIDE IMMUNOGENS
;       NUMBER OF SEQUENCES: 151
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Morgan & Finnegan, L.L.P.
;            STREET: 345 Park Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10154-0054
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC Windows
;            SOFTWARE: Word 97
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/701,588C
;            FILING DATE: 29-No. 6713301-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/100,414
;            FILING DATE: 20-JUNE-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Maria H. Lin
;            REGISTRATION NUMBER: 29,323
;            REFERENCE/DOCKET NUMBER: 1151-4158PC1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 212-758-4800
;            TELEFAX: 212-751-6849
;   INFORMATION FOR SEQ ID NO: 45:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 45 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-701-588C-45

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  Best Local Similarity   91.1%;  Pred. No. 3.4e-27;
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RESULT 7
US-08-446-692-40
; Sequence 40, Application US/08446692
; Patent No. 5759551
;  GENERAL INFORMATION:
;    APPLICANT:  Ladd, Anna
;    APPLICANT:  Wang, Chang Yi
;    APPLICANT:  Zamb, Timothy
;    TITLE OF INVENTION:  Immunogenic LHRH peptide constructs
;    TITLE OF INVENTION:  and synthetic universal immune stimulators for vaccines
;    NUMBER OF SEQUENCES:  114
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maria C.H. Lin
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10154-0053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 19
; OTHER INFORMATION: /note="D0.50;E0.50"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 20
; OTHER INFORMATION: /note="L0.25;I0.25;V0.25;F0.25"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 22
; OTHER INFORMATION: /note="E0.50;D0.50"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 23
; OTHER INFORMATION: /note="L0.25;I0.25;V0.25;F0.25"
; FEATURE:
; NAME/KEY: Modified-site
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; NAME/KEY: Modified-site
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; NAME/KEY: Modified-site
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; LOCATION: 30
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; FEATURE:
; NAME/KEY: Modified-site
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; OTHER INFORMATION: /note="L0.25;I0.25;V0.25;F0.25"
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; NAME/KEY: Modified-site
; LOCATION: 32
; OTHER INFORMATION: /note="E0.50;D0.50"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 34
; OTHER INFORMATION: /note="L0.25;I0.25;V0.25;F0.25"
US-08-446-692-40

Query Match 89.1%; Score 216.5; DB 1; Length 46;
Best Local Similarity 84.8%; Pred. No. 1.8e-24;
Matches 39; Conservative 6; Mismatches 0; Indels 1; Gaps 1;

Qy 1 TAKSKKFPSYTATYQFGG-LSEIKGVIVHRLEGVGGEHWSYGLRPG 45
Db 1 TAKSKKFPSYTATYQFGGDLSELKGLLLHKLEGLGGEHWSYGLRPG 46

RESULT 8
US-08-488-351A-40
; Sequence 40, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 19
; OTHER INFORMATION: /note="D0.50;E0.50"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 20
; OTHER INFORMATION: /note="L0.25;I0.25;V0.25;F0.25"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 22
; OTHER INFORMATION: /note="E0.50;D0.50"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 23
; OTHER INFORMATION: /note="L0.25;I0.25;V0.25;F0.25"

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;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  24
;       OTHER INFORMATION:  /note="K0.50;R0.50"
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  26
;       OTHER INFORMATION:  /note="L0.25;I0.25;V0.25;F0.25"
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  27
;       OTHER INFORMATION:  /note="L0.25;I0.25;V0.25;F0.25"
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  28
;       OTHER INFORMATION:  /note="L0.25;I0.25;V0.25;F0.25"
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  30
;       OTHER INFORMATION:  /note="K0.50;R0.50"
;     FEATURE:
;       NAME/KEY:  Modified-site
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;       NAME/KEY:  Modified-site
;       LOCATION:  32
;       OTHER INFORMATION:  /note="E0.50;D0.50"
;     FEATURE:
;       NAME/KEY:  Modified-site
;       LOCATION:  34
;       OTHER INFORMATION:  /note="L0.25;I0.25;V0.25;F0.25"
US-08-488-351A-40

  Query Match             89.1%;  Score 216.5;  DB 2;  Length 46;
  Best Local Similarity   84.8%;  Pred. No. 1.8e-24;
  Matches   39;  Conservative    6;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 TAKSKKFPSYTATYQFGG-LSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||| ||||:||:::|:|||:|||||||||||
Db          1 TAKSKKFPSYTATYQFGGDLSELKGLLLHKLEGLGGEHWSYGLRPG 46


RESULT 9
US-09-100-414B-57
; Sequence 57, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  49 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-57

  Query Match             87.7%;  Score 213;  DB 3;  Length 49;
  Best Local Similarity   83.7%;  Pred. No. 6.3e-24;
  Matches   41;  Conservative    4;  Mismatches    0;  Indels    4;  Gaps    2;

Qy          1 TAKSKKFPSYTATYQFGG--LSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
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Db          1 TAKSKKFPSYTATYQFGGISISEIKGVIVHKIEGILFGGEHWSYGLRPG 49


RESULT 10
US-09-303-323-57
; Sequence 57, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  49 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-57

  Query Match             87.7%;  Score 213;  DB 3;  Length 49;
  Best Local Similarity   83.7%;  Pred. No. 6.3e-24;
  Matches   41;  Conservative    4;  Mismatches    0;  Indels    4;  Gaps    2;

Qy          1 TAKSKKFPSYTATYQFGG--LSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
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Db          1 TAKSKKFPSYTATYQFGGISISEIKGVIVHKIEGILFGGEHWSYGLRPG 49


RESULT 11
US-09-770-014-57
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; Sequence 57, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  49 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-57

  Query Match             87.7%;  Score 213;  DB 4;  Length 49;
  Best Local Similarity   83.7%;  Pred. No. 6.3e-24;
  Matches   41;  Conservative    4;  Mismatches    0;  Indels    4;  Gaps    2;

Qy          1 TAKSKKFPSYTATYQFGG--LSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
              |||||||||||||||||  :|||||||||::||:  ||||||||||||
Db          1 TAKSKKFPSYTATYQFGGISISEIKGVIVHKIEGILFGGEHWSYGLRPG 49


RESULT 12
US-09-701-588C-57
; Sequence 57, Application US/09701588C
; Patent No. 6713301
;   GENERAL INFORMATION:
;        APPLICANT: UNITED BIOMEDICAL INC., ET AL.
;        TITLE OF INVENTION: ARTIFICIAL T HELPER CELL
;                            EPITOPES AS IMMUNE STIMULATORS FOR SYNTHETIC
;                            EPTIDE IMMUNOGENS
;        NUMBER OF SEQUENCES: 151
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Morgan & Finnegan, L.L.P.
;             STREET: 345 Park Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10154-0054
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC Windows
;             SOFTWARE: Word 97
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/701,588C
;             FILING DATE: 29-No. 6713301-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/100,414
;             FILING DATE: 20-JUNE-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maria H. Lin
;             REGISTRATION NUMBER: 29,323
;             REFERENCE/DOCKET NUMBER: 1151-4158PC1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 212-758-4800
;             TELEFAX: 212-751-6849
;   INFORMATION FOR SEQ ID NO: 57:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 49 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-701-588C-57

  Query Match             87.7%;  Score 213;  DB 4;  Length 49;
  Best Local Similarity   83.7%;  Pred. No. 6.3e-24;
  Matches   41;  Conservative    4;  Mismatches    0;  Indels    4;  Gaps    2;

Qy          1 TAKSKKFPSYTATYQFGG--LSEIKGVIVHRLEGV--GGEHWSYGLRPG 45
              |||||||||||||||||  :|||||||||::||:  ||||||||||||
Db          1 TAKSKKFPSYTATYQFGGISISEIKGVIVHKIEGILFGGEHWSYGLRPG 49


RESULT 13
US-09-100-414B-52
; Sequence 52, Application US/09100414B
; Patent No. 6025468
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/100,414B
;      FILING DATE:  20-JUNE-1998
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-100-414B-52

  Query Match             86.8%;  Score 211;  DB 3;  Length 45;
  Best Local Similarity   88.9%;  Pred. No. 1.1e-23;
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  Matches   40;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
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Db          1 TAKSKKFPSYTATYQFGGLTEIRTVIVTRLETVGGEHWSYGLRPG 45


RESULT 14
US-09-303-323-52
; Sequence 52, Application US/09303323
; Patent No. 6228987
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/303,323
;      FILING DATE:  30-APR-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-303-323-52

  Query Match             86.8%;  Score 211;  DB 3;  Length 45;
  Best Local Similarity   88.9%;  Pred. No. 1.1e-23;
  Matches   40;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||||:||: ||| ||| ||||||||||||
Db          1 TAKSKKFPSYTATYQFGGLTEIRTVIVTRLETVGGEHWSYGLRPG 45


RESULT 15
US-09-770-014-52
; Sequence 52, Application US/09770014
; Patent No. 6559282
;  GENERAL INFORMATION:
;    APPLICANT:  Wang, Chang Yi
;    TITLE OF INVENTION:  NOVEL LHRH PEPTIDE
;    TITLE OF INVENTION:  IMMUNOGENS
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morgan & Finnegan, L.L.P.
;      STREET:  345 Park Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10154-0054
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC Windows
;      SOFTWARE:  Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/770,014
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/100,414
;      FILING DATE:  20-JUNE-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maria H. Lin
;      REGISTRATION NUMBER:  29,323
;      REFERENCE/DOCKET NUMBER:  1151-4157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-758-4800
;      TELEFAX:  212-751-6849
;  INFORMATION FOR SEQ ID NO:  52:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-770-014-52

  Query Match             86.8%;  Score 211;  DB 4;  Length 45;
  Best Local Similarity   88.9%;  Pred. No. 1.1e-23;
  Matches   40;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||||:||: ||| ||| ||||||||||||
Db          1 TAKSKKFPSYTATYQFGGLTEIRTVIVTRLETVGGEHWSYGLRPG 45


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Job time : 44 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 17:21:18 ; Search time 128 Seconds
(without alignments)
114.505 Million cell updates/sec

Title: US-10-076-674A-9
Perfect score: 243
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Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	243	100.0	45	15	US-10-355-161A-9	Sequence 9, Appli
3	157	64.6	45	14	US-10-076-674-8	Sequence 8, Appli
4	157	64.6	45	15	US-10-355-161A-8	Sequence 8, Appli
5	116	47.7	31	9	US-09-848-834A-9	Sequence 9, Appli
6	116	47.7	47	9	US-09-848-834A-17	Sequence 17, Appl
7	84	34.6	16	10	US-09-747-802-72	Sequence 72, Appl
8	84	34.6	16	15	US-10-296-734-1467	Sequence 1467, Ap
9	84	34.6	16	16	US-10-789-619-72	Sequence 72, Appl
10	84	34.6	25	15	US-10-411-544-32	Sequence 32, Appl
11	79	32.5	36	14	US-10-351-641-505	Sequence 505, App
12	79	32.5	438	15	US-10-267-682-105	Sequence 105, App
13	79	32.5	438	15	US-10-267-748-105	Sequence 105, App
14	79	32.5	550	9	US-09-873-233A-18	Sequence 18, Appl
15	79	32.5	550	9	US-09-873-233A-20	Sequence 20, Appl
16	72	29.6	15	10	US-09-747-802-16	Sequence 16, Appl
17	72	29.6	15	10	US-09-747-802-30	Sequence 30, Appl
18	72	29.6	15	10	US-09-865-294-8	Sequence 8, Appli
19	72	29.6	15	10	US-09-865-294-22	Sequence 22, Appl
20	72	29.6	15	14	US-10-261-446-20	Sequence 20, Appl
21	72	29.6	15	15	US-10-411-544-10	Sequence 10, Appl
22	72	29.6	15	15	US-10-261-445B-20	Sequence 20, Appl
23	72	29.6	15	16	US-10-789-619-16	Sequence 16, Appl
24	72	29.6	15	16	US-10-789-619-30	Sequence 30, Appl
25	72	29.6	15	16	US-10-782-234-20	Sequence 20, Appl
26	72	29.6	16	9	US-09-848-834A-8	Sequence 8, Appli
27	72	29.6	18	14	US-10-351-641-1148	Sequence 1148, Ap
28	72	29.6	34	9	US-09-848-834A-13	Sequence 13, Appl
29	72	29.6	438	15	US-10-267-682-93	Sequence 93, Appl
30	72	29.6	438	15	US-10-267-748-93	Sequence 93, Appl
31	72	29.6	662	10	US-09-951-061A-141	Sequence 141, App
32	72	29.6	662	15	US-10-670-695-36	Sequence 36, Appl
33	71	29.2	284	15	US-10-358-083-6	Sequence 6, Appli
34	71	29.2	600	15	US-10-282-122A-45023	Sequence 45023, A
35	70	28.8	40	14	US-10-223-711-11	Sequence 11, Appl
36	70	28.8	986	9	US-09-870-759-33	Sequence 33, Appl
37	70	28.8	986	10	US-09-751-708A-33	Sequence 33, Appl
38	69	28.4	15	10	US-09-747-802-37	Sequence 37, Appl
39	69	28.4	15	10	US-09-865-294-29	Sequence 29, Appl
40	69	28.4	15	16	US-10-789-619-37	Sequence 37, Appl
41	69	28.4	19	10	US-09-747-802-48	Sequence 48, Appl
42	69	28.4	19	10	US-09-865-294-40	Sequence 40, Appl
43	69	28.4	19	16	US-10-789-619-48	Sequence 48, Appl
44	69	28.4	20	10	US-09-964-201A-29	Sequence 29, Appl
45	69	28.4	20	10	US-09-964-201A-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-076-674-9
; Sequence 9, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Human
US-10-076-674-9

Query Match 100.0%; Score 243; DB 14; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.3e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
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RESULT 2
US-10-355-161A-9
; Sequence 9, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A

; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Human
US-10-355-161A-9

Query Match 100.0%; Score 243; DB 15; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.3e-26;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
||||||||||||||||||||||||||||||||||||||||||||
Db 1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45

RESULT 3
US-10-076-674-8
; Sequence 8, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Human
US-10-076-674-8

Query Match 64.6%; Score 157; DB 14; Length 45;
Best Local Similarity 66.7%; Pred. No. 3e-14;
Matches 30; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
|||||||||||||||||| : :: ||||||||||||
Db 1 TAKSKKFPSYTATYQFGGFFLLTRILTIPQSLEGGEHWSYGLRPG 45

RESULT 4
US-10-355-161A-8
; Sequence 8, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Human
US-10-355-161A-8

Query Match 64.6%; Score 157; DB 15; Length 45;
Best Local Similarity 66.7%; Pred. No. 3e-14;
Matches 30; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy 1 TAKSKKFPSYTATYQFGGLSEIKGVIVHRLEGVGGEHWSYGLRPG 45
|||||||||||||||||| : :: ||||||||||||
Db 1 TAKSKKFPSYTATYQFGGFFLLTRILTIPQSLEGGEHWSYGLRPG 45

RESULT 5
US-09-848-834A-9
; Sequence 9, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide made up of amino acid sequence 288-302 of the Me
; OTHER INFORMATION: asels virus fusion protein, F linked by a spacer peptide to amino
; OTHER INFORMATION: acid sequence 2-10 of the GnRH hormone
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Amidated Lysine
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Peptide corresponds to the amino acid sequences 288-302 of the
; OTHER INFORMATION: measles virus fusion protein, F
; NAME/KEY: PEPTIDE
; LOCATION: (19)..(22)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (23)..(31)
; OTHER INFORMATION: Peptide corresponds to amino acid sequences 2-10 of the human
; OTHER INFORMATION: GnRH hormone
; NAME/KEY: MOD_RES
; LOCATION: (31)..(31)
; OTHER INFORMATION: Amidated glycine or glycinamide
US-09-848-834A-9

Query Match 47.7%; Score 116; DB 9; Length 31;
Best Local Similarity 85.7%; Pred. No. 9.7e-09;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 19 LSEIKGVIVHRLEGVGGE--HWSYGLRP 44
|||||||||||||||| | ||||||||
Db 3 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 30

RESULT 6
US-09-848-834A-17
; Sequence 17, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the Gn

```
;   OTHER INFORMATION: RH hormone linked by a spacer to amino acid sequence 288-302 of
;   OTHER INFORMATION: the Measles virus protein F linked by a spacer to amino acid seq
;   OTHER INFORMATION: uence 2-10 of the GnRH hormone
;   NAME/KEY: MOD_RES
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
;   NAME/KEY: MOD_RES
;   LOCATION: (47)..(47)
;   OTHER INFORMATION: Amidated-glycine or glycinamide
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(10)
;   OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
;   NAME/KEY: PEPTIDE
;   LOCATION: (11)..(18)
;   OTHER INFORMATION: Spacer peptide
;   NAME/KEY: PEPTIDE
;   LOCATION: (19)..(34)
;   OTHER INFORMATION: Amino acid sequence 288-302 of the Measles virus fusion protein,
;   NAME/KEY: PEPTIDE
;   LOCATION: (35)..(38)
;   OTHER INFORMATION: Spacer peptide
;   NAME/KEY: PEPTIDE
;   LOCATION: (39)..(47)
;   OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-17

  Query Match            47.7%;  Score 116;  DB 9;  Length 47;
  Best Local Similarity  85.7%;  Pred. No. 1.6e-08;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    2;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGVGGE--HWSYGLRP 44
              |||||||||||||||  |   ||||||||
Db         19 LSEIKGVIVHRLEGVEGPSLHWSYGLRP 46


RESULT 7
US-09-747-802-72
; Sequence 72, Application US/09747802
; Publication No. US20030027979A1
; GENERAL INFORMATION:
;  APPLICANT: WANG, CHANG YI
;  TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITION AS IMMUNOGENS FOR
;  TITLE OF INVENTION:  PREVENTION OF URINARY TRACT INFECTION
;  FILE REFERENCE: 1151-4165
;  CURRENT APPLICATION NUMBER: US/09/747,802
;  CURRENT FILING DATE:  2000-12-22
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Yersinia pseudotuberculosis
US-09-747-802-72

  Query Match            34.6%;  Score 84;  DB 10;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 0.00013;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQF 16
              ||||||||||||||||
Db          1 TAKSKKFPSYTATYQF 16


RESULT 8
US-10-296-734-1467
; Sequence 1467, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Scott A
;  APPLICANT:  Ramshaw, Ian A
;  TITLE OF INVENTION: Synthetic molecules and uses therefor
;  FILE REFERENCE: Savine
;  CURRENT APPLICATION NUMBER: US/10/296,734
;  CURRENT FILING DATE:  2003-08-04
;  PRIOR APPLICATION NUMBER: AU PQ7761/00
;  PRIOR FILING DATE: 2000-05-26
;  NUMBER OF SEQ ID NOS: 1507
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1467
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Invasin immunostimulatory domain
US-10-296-734-1467

  Query Match            34.6%;  Score 84;  DB 15;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 0.00013;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQF 16
              ||||||||||||||||
Db          1 TAKSKKFPSYTATYQF 16


RESULT 9
US-10-789-619-72
; Sequence 72, Application US/10789619
; Publication No. US20040141993A1
; GENERAL INFORMATION:
;  APPLICANT: WANG, CHANG YI
;  TITLE OF INVENTION: SYNTHETIC PEPTIDE COMPOSITION AS IMMUNOGENS FOR
;  TITLE OF INVENTION:  PREVENTION OF URINARY TRACT INFECTION
;  FILE REFERENCE: 1151-4165
;  CURRENT APPLICATION NUMBER: US/10/789,619
;  CURRENT FILING DATE:  2004-02-27
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Yersinia pseudotuberculosis
US-10-789-619-72

  Query Match            34.6%;  Score 84;  DB 16;  Length 16;
  Best Local Similarity  100.0%;  Pred. No. 0.00013;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQF 16
              ||||||||||||||||
Db          1 TAKSKKFPSYTATYQF 16


RESULT 10
US-10-411-544-32
; Sequence 32, Application US/10411544
; Publication No. US20030232758A1
; GENERAL INFORMATION:
;  APPLICANT: St. George-Hyslop, Peter
;  APPLICANT:  McLaurin, JoAnne
;  TITLE OF INVENTION: Immunological Methods and Compositions for the Treatment of Alzh
;  TITLE OF INVENTION:  Disease
;  FILE REFERENCE: LI01547
;  CURRENT APPLICATION NUMBER: US/10/411,544
;  CURRENT FILING DATE:  2003-04-10
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 25
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: chimeric sequence
US-10-411-544-32

  Query Match            34.6%;  Score 84;  DB 15;  Length 25;
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  Best Local Similarity   100.0%;  Pred. No. 0.00021;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          19 LSEIKGVIVHRLEGVGG 35
               |||||||||||||||||
Db           1 LSEIKGVIVHRLEGVGG 17


RESULT 11
US-10-351-641-505
; Sequence 505, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
;  APPLICANT: Barney, S.
;  APPLICANT:  Guthrie, K.
;  APPLICANT:  Merutka, G.
;  APPLICANT:  Anwer, M.
;  APPLICANT:  Lambert, D.
;  TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;  TITLE OF INVENTION:  PROPERTIES
;  FILE REFERENCE: 7872-100
;  CURRENT APPLICATION NUMBER: US/10/351,641
;  CURRENT FILING DATE:  2003-01-24
;  PRIOR APPLICATION NUMBER: 09/350,641
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/315,304
;  PRIOR FILING DATE: 1999-05-20
;  PRIOR APPLICATION NUMBER: 09/082,279
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 1757
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 505
;  LENGTH: 36
;  TYPE: PRT
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Core polypeptide
US-10-351-641-505

  Query Match             32.5%;  Score 79;  DB 14;  Length 36;
  Best Local Similarity   70.8%;  Pred. No. 0.0016;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy          19 LSEIKGVIVHRLEGV----GGEHW 38
               |||||||||||||||    | : |
Db          13 LSEIKGVIVHRLEGVSYNIGSQEW 36


RESULT 12
US-10-267-682-105
; Sequence 105, Application US/10267682
; Publication No. US20040033235A1
;  GENERAL INFORMATION:
;       APPLICANT: Bolognesi, Dani P.
;                  Matthews, Thomas J.
;                  Wild, Carl T.
;                  Barney, Shawn O.
;                  Lambert, Dennis M.
;                  Petteway, Stephen R.
;                  Langlois, Alphonse J.
;       TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
;                           MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
;                           TRANSMISSION
;       NUMBER OF SEQUENCES: 239
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/267,682
;            FILING DATE: 08-Oct-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/484,223A
;            FILING DATE: 07-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Coruzzi, Laura A.
;            REGISTRATION NUMBER: 30,742
;            REFERENCE/DOCKET NUMBER: 7872-029
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 790-9090
;            TELEFAX: (212) 869-9741/8864
;            TELEX: 66141 PENNIE
;       INFORMATION FOR SEQ ID NO: 105:
;            SEQUENCE CHARACTERISTICS:
;                 LENGTH: 438 amino acids
;                 TYPE: amino acid
;                 STRANDEDNESS: <Unknown>
;                 TOPOLOGY: unknown
;            MOLECULE TYPE: protein
;            SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-267-682-105

  Query Match
  Best Local Similarity   32.5%;  Score 79;  DB 15;  Length 438;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy          19 LSEIKGVIVHRLEGV----GGEHW 38
               |||||||||||||||    | : |
Db         176 LSEIKGVIVHRLEGVSYNIGSQEW 199


RESULT 13
US-10-267-748-105
; Sequence 105, Application US/10267748
; Publication No. US20040052820A1
;  GENERAL INFORMATION:
;       APPLICANT: Bolognesi, Dani P.
;                  Matthews, Thomas J.
;                  Wild, Carl T.
;                  Barney, Shawn O.
;                  Lambert, Dennis M.
;                  Petteway, Stephen R.
;                  Langlois, Alphonse J.
;       TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
;                           MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
;                           TRANSMISSION
;       NUMBER OF SEQUENCES: 239
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pennie & Edmonds
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: New York
;            COUNTRY: USA
;            ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/267,748
;            FILING DATE: 08-Oct-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/484,223A
;            FILING DATE: 07-JUN-1995
;       ATTORNEY/AGENT INFORMATION
```

```
;             NAME: Coruzzi, Laura A.
;             REGISTRATION NUMBER: 30,742
;             REFERENCE/DOCKET NUMBER: 7872-029
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 790-9090
;             TELEFAX: (212) 869-9741/8864
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 105:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 438 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: unknown
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-267-748-105

  Query Match             32.5%;  Score 79;  DB 15;  Length 438;
  Best Local Similarity   70.8%;  Pred. No. 0.029;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        176 LSEIKGVIVHRLEGVSYNIGSQEW 199


RESULT 14
US-09-873-233A-18
; Sequence 18, Application US/09873233A
; Patent No. US20020146434A1
; GENERAL INFORMATION:
;  APPLICANT: UEDA, Shigeharu
;  APPLICANT:  WATANABE, Michiko
;  APPLICANT:  KAWANISHI, Hitomi
;  TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN
;  FILE REFERENCE: 0216-0451P
;  CURRENT APPLICATION NUMBER: US/09/873,233A
;  CURRENT FILING DATE:  2001-06-05
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 550
;   TYPE: PRT
;   ORGANISM: Measles virus
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (1)..(550)
;   OTHER INFORMATION: any n or Xaa = Unknown
US-09-873-233A-18

  Query Match             32.5%;  Score 79;  DB 9;  Length 550;
  Best Local Similarity   70.8%;  Pred. No. 0.038;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 15
US-09-873-233A-20
; Sequence 20, Application US/09873233A
; Patent No. US20020146434A1
; GENERAL INFORMATION:
;  APPLICANT: UEDA, Shigeharu
;  APPLICANT:  WATANABE, Michiko
;  APPLICANT:  KAWANISHI, Hitomi
;  TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN
;  FILE REFERENCE: 0216-0451P
;  CURRENT APPLICATION NUMBER: US/09/873,233A
;  CURRENT FILING DATE:  2001-06-05
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 550
;   TYPE: PRT
;   ORGANISM: Measles virus
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (1)..(550)
;   OTHER INFORMATION: any n or Xaa = Unknown
US-09-873-233A-20

  Query Match             32.5%;  Score 79;  DB 9;  Length 550;
  Best Local Similarity   70.8%;  Pred. No. 0.038;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


Search completed: February  8, 2005, 17:33:48
Job time : 128 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 17:18:58 ; Search time 173 Seconds
(without alignments)
133.200 Million cell updates/sec

Title: US-10-076-674A-9
Perfect score: 243
Sequence: 1 TAKSKKFPSYTATYQFGGLS.....IVHRLEGVGGEHWSYGLRPG 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	34.6	835	1	INVA_YEREN	P19196 yersinia en
2	84	34.6	835	2	Q56889	Q56889 yersinia en
3	80	32.9	546	1	VGLF_RINDB	P41360 rinderpest
4	80	32.9	546	2	Q91HA5	Q91ha5 rinderpest
5	79	32.5	531	2	Q76R52	Q76r52 measles vir
6	79	32.5	534	1	VGLF_MEASY	P26032 measles vir
7	79	32.5	534	2	Q04243	Q04243 measles vir
8	79	32.5	534	2	Q76R53	Q76r53 measles vir
9	79	32.5	537	2	Q04242	Q04242 measles vir
10	79	32.5	545	2	Q9PXA4	Q9pxa4 measles vir
11	79	32.5	546	1	VGLF_RINDR	P41356 rinderpest
12	79	32.5	550	1	VGLF_MEASA	P35973 measles vir
13	79	32.5	550	1	VGLF_MEASE	P08300 measles vir
14	79	32.5	550	2	P90330	P90330 measles vir
15	79	32.5	550	2	P90331	P90331 measles vir
16	79	32.5	550	2	Q8V049	Q8v049 measles vir
17	79	32.5	550	2	Q68KG1	Q68kg1 measles vir
18	79	32.5	550	2	Q68KG3	Q68kg3 measles vir
19	79	32.5	550	2	Q784S2	Q784s2 measles vir
20	79	32.5	550	2	Q89495	Q89495 measles vir
21	79	32.5	550	2	Q9QEW7	Q9qew7 measles vir
22	79	32.5	550	2	Q9QEW8	Q9qew8 measles vir
23	79	32.5	550	2	Q9QEW9	Q9qew9 measles vir
24	79	32.5	550	2	Q9QEX0	Q9qex0 measles vir
25	79	32.5	550	2	Q9QEX1	Q9qex1 measles vir
26	79	32.5	550	2	Q9WMK4	Q9wmk4 measles vir
27	79	32.5	550	2	Q9YJ94	Q9yj94 measles vir
28	79	32.5	553	2	O11383	O11383 measles vir
29	79	32.5	553	2	O91248	O91248 measles vir
30	79	32.5	553	2	O93055	O93055 measles vir
31	79	32.5	553	2	P88973	P88973 measles vir
32	79	32.5	553	2	P88974	P88974 measles vir
33	79	32.5	553	2	Q04244	Q04244 measles vir
34	79	32.5	553	2	Q91QP2	Q91qp2 measles vir
35	79	32.5	553	2	Q77M18	Q77m18 measles vir
36	79	32.5	553	2	Q77M34	Q77m34 measles vir
37	79	32.5	553	2	Q77M38	Q77m38 measles vir
38	79	32.5	553	2	Q83518	Q83518 measles vir
39	79	32.5	553	2	Q83521	Q83521 measles vir
40	79	32.5	553	2	Q83525	Q83525 measles vir
41	79	32.5	553	2	Q83527	Q83527 measles vir
42	79	32.5	553	2	Q83530	Q83530 measles vir
43	79	32.5	553	2	Q83533	Q83533 measles vir
44	79	32.5	553	2	Q83536	Q83536 measles vir
45	79	32.5	553	2	Q9IC36	Q9ic36 measles vir

ALIGNMENTS

RESULT 1
INVA_YEREN
ID INVA_YEREN STANDARD; PRT; 835 AA.
AC P19196;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Invasin.
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8081C / Serotype O:8;
RX MEDLINE=91041720; PubMed=2233250;
RA Young V.B., Miller V.L., Falkow S., Schoolnik G.K.;
RT "Sequence, localization and function of the invasin protein of
RT Yersinia enterocolitica.";
RL Mol. Microbiol. 4:1119-1128(1990).
CC -!- FUNCTION: Invasin is a protein that allows enteric bacteria to
CC penetrate cultured mammalian cells. The entry of invasin in the
CC cell is mediated by binding several beta-1 chain integrins.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: Belongs to the intimin/invasin family.
CC --

CC --
DR EMBL; X53368; CAA37448.1; -.
DR PIR; S11442; S11442.
DR HSSP; P11922; 1CWV.
DR InterPro; IPR003344; Big_1.
DR InterPro; IPR003535; Intimin.
DR InterPro; IPR008964; Invasin_intimin.
DR Pfam; PF02369; Big_1; 1.
DR PRINTS; PR01369; INTIMIN.
DR SMART; SM00634; BID_1; 1.
KW Outer membrane.
SQ SEQUENCE 835 AA; 91361 MW; 6133FF9FDB8D9BBA CRC64;

Query Match 34.6%; Score 84; DB 1; Length 835;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TAKSKKFPSYTATYQF 16
              ||||||||||||||||
Db        718 TAKSKKFPSYTATYQF 733
```

```
RESULT 2
Q56889
ID   Q56889      PRELIMINARY;      PRT;   835 AA.
AC   Q56889;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Invasin.
GN   Name=invA;
OS   Yersinia enterocolitica.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Yersinia.
OX   NCBI_TaxID=630;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=W1024;
RX   MEDLINE=94195100; PubMed=7511772;
RA   Pepe J.C., Badger J.L., Miller V.L.;
RT   "Growth phase and low pH affect the thermal regulation of the Yersinia
RT   enterocolitica inv gene.";
RL   Mol. Microbiol. 11:123-135(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=W1024;
RX   MEDLINE=98048470; PubMed=9387224;
RA   Fauconnier A., Allaoui A., Campos A., Van Elsen A., Cornelis G.R.,
RA   Bollen A.;
RT   "Flagellar flhA, flhB and flhE genes, organized in an operon, cluster
RT   upstream from the inv locus in Yersinia enterocolitica.";
RL   Microbiology 143:3461-3471(1997).
DR   EMBL; Z48169; CAA88188.1; -.
DR   PIR; S54216; S54216.
DR   HSSP; P11922; 1CWV.
DR   GO; GO:0007155; P:cell adhesion; IEA.
DR   InterPro; IPR003344; Big_1.
DR   InterPro; IPR003535; Intimin.
DR   InterPro; IPR008964; Invasin_intimin.
DR   Pfam; PF02369; Big_1; 1.
DR   PRINTS; PR01369; INTIMIN.
SQ   SEQUENCE   835 AA;  91367 MW;  C817F6D7766184E3 CRC64;

  Query Match             34.6%;  Score 84;  DB 2;  Length 835;
  Best Local Similarity   100.0%;  Pred. No. 0.029;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TAKSKKFPSYTATYQF 16
              ||||||||||||||||
Db        718 TAKSKKFPSYTATYQF 733


RESULT 3
VGLF_RINDB
ID   VGLF_RINDB      STANDARD;      PRT;   546 AA.
AC   P41360;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   Name=F;
OS   Rinderpest virus (strain RBT1) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=39007;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z31656; CAA83482.1; -.
DR   PIR; S47300; S47300.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein; Glycoprotein; Signal; Transmembrane.
FT   SIGNAL       1     19
FT   CHAIN       20    546       Fusion glycoprotein F0.
FT   CHAIN       20    108       Fusion glycoprotein F2.
FT   CHAIN      109    546       Fusion glycoprotein F1.
FT   DOMAIN     104    108       Arg/Lys-rich (basic).
FT   TRANSMEM   109    133       Potential.
FT   TRANSMEM   484    513       Potential.
FT   DOMAIN     514    517       Arg/Lys-rich (basic).
FT   DISULFID    64    191       Linkage between F2 and F1 (Potential).
FT   CARBOHYD    25     25       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    57     57       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    63     63       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD   518    518       O-linked (Potential).
SQ   SEQUENCE   546 AA;  58418 MW;  38B539B89344F401 CRC64;

  Query Match             32.9%;  Score 80;  DB 1;  Length 546;
  Best Local Similarity   63.0%;  Pred. No. 0.064;
  Matches   17;  Conservative    2;  Mismatches    4;  Indels    4;  Gaps    1;

Qy         16 FGGLSEIKGVIVHRLEGV----GGEHW 38
              :  ||||||||||||||||    | : |
Db        281 YPSLSEIKGVIVHRLEGVSYNIGSQEW 307


RESULT 4
Q91HA5
ID   Q91HA5      PRELIMINARY;      PRT;   546 AA.
AC   Q91HA5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fusion protein.
OS   Rinderpest virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11241;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K;
RX   MEDLINE=21014265; PubMed=11186456;
RA   Aianot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RA   Gusev A.A.;
RT   "Primary structure of the F-gene from Rinderpest virus strain K.";
RL   Mol. Genet. Mikrobiol. Virusol. 4:29-33(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K;
RA   Ayanot P.K., Sminev A.G., Bezborodova S.V., Starov S.K., Drygin V.V.,
RA   Gusev A.A.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
```

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DR   EMBL; AY035887; AAK63190.1; -.
DR   PIR; PQ0866; PQ0866.
DR   PIR; PQ0867; PQ0867.
DR   PIR; PQ0873; PQ0873.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein.
SQ   SEQUENCE   546 AA;  58571 MW;  449B2B2DD7405F0B CRC64;

  Query Match             32.9%;  Score 80;  DB 2;  Length 546;
  Best Local Similarity   63.0%;  Pred. No. 0.064;
  Matches   17;  Conservative    2;  Mismatches    4;  Indels    4;  Gaps    1;

Qy         16 FGGLSEIKGVIVHRLEGV----GGEHW 38
              :  |||||||||||||||    | : |
Db        281 YPSLSEIKGVIVHRLEGVSYNIGSQEW 307


RESULT 5
Q76R52
ID   Q76R52      PRELIMINARY;      PRT;   531 AA.
AC   Q76R52;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cattaneo R., Billeter M.A.;
RT   "Mutated and hypermutated genes of persistent measles viruses which
RT   caused lethal human brain diseases.";
RL   Virology 0:0-0(0).
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
DR   EMBL; X16568; CAA34582.1; -.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein.
SQ   SEQUENCE   531 AA;  57568 MW;  AF0F45F7AD80D1D3 CRC64;

  Query Match             32.5%;  Score 79;  DB 2;  Length 531;
  Best Local Similarity   70.8%;  Pred. No. 0.085;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 6
VGLF_MEASY
ID   VGLF_MEASY     STANDARD;      PRT;   534 AA.
AC   P26032;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   Name=F;
OS   Measles virus (strain Yamagata-1) (Subacute sclerose panencephalitis
OS   virus).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11239;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90385702; PubMed=1698327;
RA   Komase K., Haga T., Yoshikawa Y., Sato T.A., Yamanouchi K.;
RT   "Molecular analysis of structural protein genes of the Yamagata-1
RT   strain of defective subacute sclerosing panencephalitis virus. IV.
RT   Nucleotide sequence of the fusion gene.";
RL   Virus Genes 4:173-181(1990).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10548; BAA01405.1; -.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein; Glycoprotein; Signal; Transmembrane.
FT   SIGNAL        1     23
FT   CHAIN        24    534       Fusion glycoprotein F0.
FT   CHAIN        24    112       Fusion glycoprotein F2.
FT   CHAIN       113    534       Fusion glycoprotein F1.
FT   TRANSMEM    113    136       Potential.
FT   DOMAIN      137    494       Extracellular (Potential).
FT   TRANSMEM    495    515       Potential.
FT   DOMAIN      516    534       Cytoplasmic (Potential).
FT   DISULFID     68    195       Linkage between F2 and F1 (Potential).
FT   CARBOHYD     29     29       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     61     61       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     67     67       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   534 AA;  57963 MW;  F5B21757E643844D CRC64;

  Query Match             32.5%;  Score 79;  DB 1;  Length 534;
  Best Local Similarity   70.8%;  Pred. No. 0.085;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 7
Q04243
ID   Q04243      PRELIMINARY;      PRT;   534 AA.
AC   Q04243;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cattaneo R., Billeter M.A.;
RT   "Mutated and hypermutated genes of persistent measles viruses which
RT   caused lethal human brain diseases.";
RL   Virology 0:0-0(0).
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
```

```
DR   EMBL; X16568; CAA34581.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein.
SQ   SEQUENCE   534 AA;  57900 MW;  637245E23B5BE044 CRC64;

  Query Match             32.5%;  Score 79;  DB 2;  Length 534;
  Best Local Similarity   70.8%;  Pred. No. 0.085;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        291 LSEIKGVIVHRLEGVSYNIGSQEW 314


RESULT 8
Q76R53
ID   Q76R53      PRELIMINARY;      PRT;   534 AA.
AC   Q76R53;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cattaneo R., Billeter M.A.;
RT   "Mutated and hypermutated genes of persistent measles viruses which
RT   caused lethal human brain diseases.";
RL   Virology 0:0-0(0).
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
DR   EMBL; X16567; CAA34575.1; -.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein.
SQ   SEQUENCE   534 AA;  57944 MW;  70DA7D1A10978B90 CRC64;

  Query Match             32.5%;  Score 79;  DB 2;  Length 534;
  Best Local Similarity   70.8%;  Pred. No. 0.085;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 9
Q04242
ID   Q04242      PRELIMINARY;      PRT;   537 AA.
AC   Q04242;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cattaneo R., Billeter M.A.;
RT   "Mutated and hypermutated genes of persistent measles viruses which
RT   caused lethal human brain diseases.";
RL   Virology 0:0-0(0).
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
DR   EMBL; X16567; CAA34574.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein.
SQ   SEQUENCE   537 AA;  58275 MW;  D0A60AC66D979E06 CRC64;

  Query Match             32.5%;  Score 79;  DB 2;  Length 537;
  Best Local Similarity   70.8%;  Pred. No. 0.086;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        291 LSEIKGVIVHRLEGVSYNIGSQEW 314


RESULT 10
Q9PXA4
ID   Q9PXA4      PRELIMINARY;      PRT;   545 AA.
AC   Q9PXA4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OSA-3;
RX   MEDLINE=22072939; PubMed=12076836; DOI=10.1016/S0168-1702(02)00042-4;
RA   Ning X., Ayata M., Kimura M., Komase K., Furukawa K., Seto T., Ito N.,
RA   Shingai M., Matsunaga I., Yamano T., Ogura H.;
RT   "Alterations and diversity in the cytoplasmic tail of the fusion
RT   protein of subacute sclerosing panencephalitis virus strains isolated
RT   in Osaka, Japan.";
RL   Virus Res. 86:123-131(2002).
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
DR   EMBL; AF179440; AAF02705.1; -.
DR   EMBL; AF179439; AAF02704.1; -.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein.
SQ   SEQUENCE   545 AA;  58907 MW;  0234C28AE193E77D CRC64;

  Query Match             32.5%;  Score 79;  DB 2;  Length 545;
  Best Local Similarity   70.8%;  Pred. No. 0.087;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 11
VGLF_RINDR
ID   VGLF_RINDR      STANDARD;      PRT;   546 AA.
AC   P41356;
```

```
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   Name=F;
OS   Rinderpest virus (strain RBOK) (RDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=36409;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95088609; PubMed=7996154;
RA   Evans S.A., Baron M.D., Chamberlain R.W., Goatley L., Barrett T.;
RT   "Nucleotide sequence comparisons of the fusion protein gene from
RT   virulent and attenuated strains of rinderpest virus.";
RL   J. Gen. Virol. 75:3611-3617(1994).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z30700; CAA83186.1; -.
DR   EMBL; Z30697; CAA83181.1; -.
DR   PIR; S47305; S47305.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein; Glycoprotein; Signal; Transmembrane.
FT   SIGNAL        1     19
FT   CHAIN        20    546       Fusion glycoprotein F0.
FT   CHAIN        20    108       Fusion glycoprotein F2.
FT   CHAIN       109    546       Fusion glycoprotein F1.
FT   DOMAIN      104    108       Arg/Lys-rich (basic).
FT   TRANSMEM    109    133       Potential.
FT   TRANSMEM    484    513       Potential.
FT   DOMAIN      514    517       Arg/Lys-rich (basic).
FT   DISULFID     64    191       Linkage between F2 and F1 (Potential).
FT   CARBOHYD     25     25       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     57     57       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     63     63       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    518    518       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   546 AA;  58705 MW;  ED3DF8AFFDBECB95 CRC64;

  Query Match             32.5%;  Score 79;  DB 1;  Length 546;
  Best Local Similarity   59.3%;  Pred. No. 0.087;
  Matches   16;  Conservative    3;  Mismatches    4;  Indels    4;  Gaps    1;

Qy         16 FGGLSEIKGVIVHRLEGV----GGEHW 38
              :  ||||||||:||||||    | : |
Db        281 YPSLSEIKGVIIHRLEGVSYNIGSQEW 307


RESULT 12
VGLF_MEASA
ID   VGLF_MEASA     STANDARD;      PRT;   550 AA.
AC   P35973;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   Name=F;
OS   Measles virus (strain AIK-C) (Subacute sclerose panencephalitis
OS   virus).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=36408;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93227570; PubMed=8470368;
RA   Mori T., Sasaki K., Hashimoto H., Makino S.;
RT   "Molecular cloning and complete nucleotide sequence of genomic RNA of
RT   the AIK-C strain of attenuated measles virus.";
RL   Virus Genes 7:67-81(1993).
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S58435; AAB26145.1; -.
DR   PIR; E48556; E48556.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein; Glycoprotein; Signal; Transmembrane.
FT   SIGNAL        1     23
FT   CHAIN        24    550       Fusion glycoprotein F0.
FT   CHAIN        24    112       Fusion glycoprotein F2.
FT   CHAIN       113    550       Fusion glycoprotein F1.
FT   TRANSMEM    113    136       Potential.
FT   DOMAIN      137    494       Extracellular (Potential).
FT   TRANSMEM    495    515       Potential.
FT   DOMAIN      516    550       Cytoplasmic (Potential).
FT   DISULFID     68    195       Linkage between F2 and F1 (Potential).
FT   CARBOHYD     29     29       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     61     61       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     67     67       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   550 AA;  59540 MW;  AAC4DAB92DE0D938 CRC64;

  Query Match             32.5%;  Score 79;  DB 1;  Length 550;
  Best Local Similarity   70.8%;  Pred. No. 0.088;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              ||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 13
VGLF_MEASE
ID   VGLF_MEASE     STANDARD;      PRT;   550 AA.
AC   P08300;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE   Fusion glycoprotein F1].
GN   Name=F;
OS   Measles virus (strain Edmonston) (Subacute sclerose panencephalitis
OS   virus),
OS   Measles virus (strain Halle) (Subacute sclerose panencephalitis
OS   virus),
OS   Measles virus (strain Leningrad-16) (Subacute sclerose panencephalitis
OS   virus),
OS   Measles virus (strain Edmonston-Zagreb) (Subacute sclerose
OS   panencephalitis virus),
OS   Measles virus (strain Philadelphia-26) (Subacute sclerose
```

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OS   panencephalitis virus), and
OS   Measles virus (strain Edmonston B) (Subacute sclerose panencephalitis
OS   virus).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11235, 11236, 70147, 70149, 70148, 70146;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston;
RX   MEDLINE=87071668; PubMed=3788062;
RA   Richardson C.D., Hull D., Greer P., Hasel K., Berkovich A.,
RA   Englund G., Bellini W.J., Rima B., Lazzarini R.A.;
RT   "The nucleotide sequence of the mRNA encoding the fusion protein of
RT   measles virus (Edmonston strain): a comparison of fusion proteins from
RT   several different paramyxoviruses.";
RL   Virology 155:508-523(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Halle;
RX   MEDLINE=87224816; PubMed=3585281;
RA   Buckland R., Gerald C., Barker R., Wild T.F.;
RT   "Fusion glycoprotein of measles virus: nucleotide sequence of the gene
RT   and comparison with other paramyxoviruses.";
RL   J. Gen. Virol. 68:1695-1703(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston;
RX   MEDLINE=90085790; PubMed=2596022;
RA   Cattaneo R., Schmid A., Spielhofer P., Kaelin K., Baczko K.,
RA   Meulen V., Pardowitz J., Flanagan S., Rima B.K., Udem S.A.;
RT   "Mutated and hypermutated genes of persistent measles viruses which
RT   caused lethal human brain diseases.";
RL   Virology 173:415-425(1989).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston;
RX   MEDLINE=92263801; PubMed=1585658;
RA   Schmid A., Spielhofer P., Cattaneo R., Baczko K., Ter Meulen V.,
RA   Billeter M.A.;
RT   "Subacute sclerosing panencephalitis is typically characterized by
RT   alterations in the fusion protein cytoplasmic domain of the persisting
RT   measles virus.";
RL   Virology 188:910-915(1992).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston, Edmonston-Zagreb, and Leningrad-16;
RX   MEDLINE=94249283; PubMed=8191786; DOI=10.1016/0168-1702(94)90025-6;
RA   Rota J.S., Wang Z.D., Rota P.A., Bellini W.J.;
RT   "Comparison of sequences of the H, F, and N coding genes of measles
RT   virus vaccine strains.";
RL   Virus Res. 31:317-330(1994).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Philadelphia-26;
RX   MEDLINE=94303181; PubMed=8030232;
RA   Hummel K.B., Vanchiere J.A., Bellini W.J.;
RT   "Restriction of fusion protein mRNA as a mechanism of measles virus
RT   persistence.";
RL   Virology 202:665-672(1994).
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Edmonston B;
RA   Billeter M.A.;
RL   Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: This protein directs fusion of viral and cellular
CC       membranes.
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14915; AAA46423.1; -.
DR   EMBL; X05597; CAA29090.1; ALT_INIT.
DR   EMBL; K01711; AAA75498.1; ALT_INIT.
DR   EMBL; K01711; AAA75499.1; -.
DR   EMBL; U03657; AAA56647.1; ALT_INIT.
DR   EMBL; U03659; AAA56649.1; ALT_INIT.
DR   EMBL; U03670; AAA56660.1; ALT_INIT.
DR   EMBL; U08416; AAA50550.1; ALT_INIT.
DR   EMBL; Z66517; CAA91367.1; ALT_INIT.
DR   EMBL; Z66517; CAA91368.1; -.
DR   HSSP; P04849; 1SVF.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein; Glycoprotein; Signal; Transmembrane.
FT   SIGNAL        1     23
FT   CHAIN        24    550       Fusion glycoprotein F0.
FT   CHAIN        24    112       Fusion glycoprotein F2.
FT   CHAIN       113    550       Fusion glycoprotein F1.
FT   TRANSMEM    113    136       Potential.
FT   DOMAIN      137    494       Extracellular (Potential).
FT   TRANSMEM    495    515       Potential.
FT   DOMAIN      516    550       Cytoplasmic (Potential).
FT   DISULFID     68    195       Linkage between F2 and F1 (Potential).
FT   CARBOHYD     29     29       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     61     61       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     67     67       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   550 AA;  59532 MW;  7AA4F1CA82169093 CRC64;

  Query Match             32.5%;  Score 79;  DB 1;  Length 550;
  Best Local Similarity   70.8%;  Pred. No. 0.088;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 14
P90330
ID   P90330      PRELIMINARY;      PRT;   550 AA.
AC   P90330;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nagahata;
RA   Sheng J., Watanabe M., Ueda S.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nagahata;
RA   Sheng J., Nakanishi M., Watanabe M., Ueda S.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
DR   EMBL; D63924; BAA09951.1; -.
DR   PIR; PQ0376; PQ0376.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
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DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein.
SQ   SEQUENCE   550 AA;  59589 MW;  73E7BD457ABA39B7 CRC64;

  Query Match             32.5%;  Score 79;  DB 2;  Length 550;
  Best Local Similarity   70.8%;  Pred. No. 0.088;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 15
P90331
ID   P90331      PRELIMINARY;      PRT;   550 AA.
AC   P90331;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Fusion protein.
OS   Measles virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nagahata;
RA   Sheng J., Watanabe M., Ueda S.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nagahata;
RA   Sheng J., Nakanishi M., Watanabe M., Ueda S.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Nagahata;
RX   MEDLINE=22072939; PubMed=12076836; DOI=10.1016/S0168-1702(02)00042-4;
RA   Ning X., Ayata M., Kimura M., Komase K., Furukawa K., Seto T., Ito N.,
RA   Shingai M., Matsunaga I., Yamano T., Ogura H.;
RT   "Alterations and diversity in the cytoplasmic tail of the fusion
RT   protein of subacute sclerosing panencephalitis virus strains isolated
RT   in Osaka, Japan.";
RL   Virus Res. 86:123-131(2002).
CC   -!- SUBUNIT: Heterodimer of F1 and F2; disulfide-linked (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC       family.
DR   EMBL; D63926; BAA09958.1; -.
DR   EMBL; AF179431; AAF02696.1; -.
DR   PIR; PQ0376; PQ0376.
DR   HSSP; P04849; 1SVF.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   GO; GO:0006948; P:viral-induced cell-cell fusion; IEA.
DR   InterPro; IPR000776; Fusion_gly.
DR   Pfam; PF00523; Fusion_gly; 1.
KW   Envelope protein; Fusion protein.
SQ   SEQUENCE   550 AA;  59530 MW;  97C991C7E2169839 CRC64;

  Query Match             32.5%;  Score 79;  DB 2;  Length 550;
  Best Local Similarity   70.8%;  Pred. No. 0.088;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


Search completed: February  8, 2005, 17:30:50
Job time : 174 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 17:19:57 ; Search time 39 Seconds
(without alignments)
111.019 Million cell updates/sec

Title: US-10-076-674A-9
Perfect score: 243
Sequence: 1 TAKSKKFPSYTATYQFGGLS.....IVHRLEGVGGEHWSYGLRPG 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	34.6	835	1	S54216	invasin - Yersinia
2	84	34.6	835	2	S11442	invasin - Yersinia
3	80	32.9	546	2	S47300	gene F protein - r
4	79	32.5	282	2	PQ0376	cell fusion glycop
5	79	32.5	282	2	PQ0388	cell fusion glycop
6	79	32.5	534	1	JU0274	cell fusion glycop
7	79	32.5	546	1	VGNZRK	cell fusion glycop
8	79	32.5	546	2	S47305	gene F protein - r
9	79	32.5	550	1	E48556	cell fusion glycop
10	79	32.5	553	1	VGNZMV	cell fusion glycop
11	74	30.5	90	1	RHMSG	gonadoliberin prec
12	74	30.5	92	1	RHRTG	gonadoliberin prec
13	74	30.5	546	1	VGNZRL	cell fusion glycop
14	72	29.6	542	2	JQ2223	cell fusion protei
15	72	29.6	552	2	S47034	cell fusion protei
16	72	29.6	631	1	A48346	cell fusion glycop
17	72	29.6	631	1	VGNZPD	cell fusion glycop
18	72	29.6	662	1	VGNZCD	cell fusion glycop
19	72	29.6	662	2	S21382	cell fusion protei
20	71	29.2	92	1	RHHUG	gonadoliberin prec
21	70	28.8	67	2	I78541	gonadoliberin prec
22	70	28.8	986	1	A29646	invasin - Yersinia
23	67	27.6	546	2	S55386	cell fusion protei
24	64.5	26.5	265	2	T05668	pollen allergen ho
25	64	26.3	636	2	S47299	gene F protein - r
26	63.5	26.1	89	2	I51423	gonadoliberin prec
27	61	25.1	900	2	JH0157	cellulase (EC 3.2.
28	60	24.7	10	1	RHPGG	gonadoliberin - pi
29	60	24.7	10	1	RHSHG	gonadoliberin - sh
30	60	24.7	1085	2	T03531	cobN protein homol
31	59	24.3	584	2	JQ1229	cellulase (EC 3.2.
32	57	23.5	675	2	I39065	transcription init
33	56	23.0	10	1	RHAQ1	gonadoliberin I -
34	56	23.0	92	2	I50644	gonadoliberin I pr
35	56	23.0	147	2	A84546	50S ribosomal prot
36	56	23.0	162	2	T49957	ribosomal protein
37	56	23.0	187	2	T47342	hypothetical prote
38	56	23.0	473	2	T38350	threonine-tRNA lig
39	56	23.0	551	2	E64728	yabN protein - Esc
40	56	23.0	552	2	B90638	probable transport
41	56	23.0	552	2	B85489	probable transport
42	56	23.0	601	2	D83583	probable acyl-CoA
43	55.5	22.8	489	2	B69964	probable glucose-6
44	54.5	22.4	263	2	T47536	hypothetical prote
45	54.5	22.4	710	2	E69665	nitrate reductase

ALIGNMENTS

RESULT 1
S54216
invasin - Yersinia enterocolitica (strain W1024)
C;Species: Yersinia enterocolitica
A;Variety: strain W1024
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S54216
R;Fauconnier, A.; Allaoui, A.; van Elsen, A.; Cornelis, G.; Bollen, A.
submitted to the EMBL Data Library, February 1995
A;Description: Clustering of flagellar genes around invA, the Yersinia enterocolitica inv
A;Reference number: S54213
A;Accession: S54216
A;Molecule type: DNA
A;Residues: 1-835 <FAU>
A;Cross-references: UNIPROT:Q56889; EMBL:Z48169; NID:g793891; PIDN:CAA88188.1; PID:g79389
A;Experimental source: strain W1024; serotype O:9
C;Genetics:
A;Gene: invA
C;Superfamily: invasin

Query Match 34.6%; Score 84; DB 1; Length 835;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TAKSKKFPSYTATYQF 16
              ||||||||||||||||
Db        718 TAKSKKFPSYTATYQF 733
```

RESULT 2
S11442
invasin - Yersinia enterocolitica
C;Species: Yersinia enterocolitica
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11442; S71023
R;Young, V.B.; Miller, V.L.; Falkow, S.; Schoolnik, G.K.
Mol. Microbiol. 4, 1119-1128, 1990
A;Title: Sequence, localization and function of the invasin protein of Yersinia enterocol
A;Reference number: S11442; MUID:91041720; PMID:2233250
A;Accession: S11442
A;Molecule type: DNA
A;Residues: 1-835 <YOU>
A;Cross-references: UNIPROT:P19196; EMBL:X53368; NID:g48573; PIDN:CAA37448.1; PID:g48574
A;Experimental source: strain 8081c
C;Genetics:
A;Gene: invA
C;Superfamily: invasin

Query Match 34.6%; Score 84; DB 2; Length 835;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TAKSKKFPSYTATYQF 16
              ||||||||||||||||
Db        718 TAKSKKFPSYTATYQF 733
```

RESULT 3
S47300
gene F protein - rinderpest virus
C;Species: rinderpest virus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S47300; PQ0865
R;Evans, S.A.; Baron, M.D.; Chamberlain, R.W.; Goatley, L.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Description: The complete nucleotide sequence of the fusion protein gene of the vaccin
A;Reference number: S47299
A;Accession: S47300
A;Molecule type: DNA
A;Residues: 1-546 <EVA>
A;Cross-references: UNIPROT:P41360; EMBL:Z31656; NID:g535406; PIDN:CAA83482.1; PID:g5354
R;Chamberlain, R.W.; Wamwayi, H.M.; Hockley, E.; Shaila, M.S.; Goatley, L.; Knowles, N.J
J. Gen. Virol. 74, 2775-2780, 1993
A;Title: Evidence for different lineages of rinderpest virus reflecting their geographic
A;Reference number: PQ0865; MUID:94103786; PMID:8277286
A;Accession: PQ0865
A;Molecule type: mRNA
A;Residues: 86-191 <CHA>
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein

Query Match 32.9%; Score 80; DB 2; Length 546;
Best Local Similarity 63.0%; Pred. No. 0.02;
Matches 17; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

```
Qy          16 FGGLSEIKGVIVHRLEGV----GGEHW 38
               :  ||||||||||||||||    | : |
Db         281 YPSLSEIKGVIVHRLEGVSYNIGSQEW 307
```

RESULT 4
PQ0376
cell fusion glycoprotein - measles virus (strain TT) (fragment)
C;Species: measles virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: PQ0376
R;Schulz, T.F.; Hoad, J.G.; Whitby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J. Gen. Virol. 73, 1581-1586, 1992
A;Title: A measles virus isolate from a child with Kawasaki disease: sequence comparison
A;Reference number: PQ0374; MUID:92300360; PMID:1607874
A;Accession: PQ0376
A;Molecule type: genomic RNA
A;Residues: 1-282 <SCH>
A;Cross-references: UNIPROT:Q83629; UNIPROT:O93055; UNIPROT:Q9IC36; UNIPROT:P88973; UNIP
PROT:P90330; UNIPROT:Q9QEW7; UNIPROT:Q9WMK4; UNIPROT:Q83525; UNIPROT:Q83518; UNIPROT:Q89
3521; UNIPROT:Q83530; UNIPROT:O91248; UNIPROT:Q91QP2; UNIPROT:Q9QEW8; UNIPROT:Q04244
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion

Query Match 32.5%; Score 79; DB 2; Length 282;
Best Local Similarity 70.8%; Pred. No. 0.013;
Matches 17; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

```
Qy          19 LSEIKGVIVHRLEGV----GGEHW 38
               ||||||||||||||    | : |
Db         20 LSEIKGVIVHRLEGVSYNIGSQEW 43
```

RESULT 5
PQ0388
cell fusion glycoprotein - measles virus (strain Schwarz vaccine) (fragment)
C;Species: measles virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: PQ0388
R;Schulz, T.F.; Hoad, J.G.; Whitby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J. Gen. Virol. 73, 1581-1586, 1992
A;Title: A measles virus isolate from a child with Kawasaki disease: sequence compariso
A;Reference number: PQ0374; MUID:92300360; PMID:1607874
A;Accession: PQ0388
A;Molecule type: genomic RNA
A;Residues: 1-282 <SCH>
A;Cross-references: UNIPROT:Q83525; UNIPROT:Q83530
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion

Query Match 32.5%; Score 79; DB 2; Length 282;
Best Local Similarity 70.8%; Pred. No. 0.013;
Matches 17; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

```
Qy          19 LSEIKGVIVHRLEGV----GGEHW 38
               ||||||||||||||    | : |
Db         20 LSEIKGVIVHRLEGVSYNIGSQEW 43
```

RESULT 6
JU0274
cell fusion glycoprotein precursor - subacute sclerosing panencephalitis virus (strain Y
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: subacute sclerosing panencephalitis virus, SSPEV
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000
C;Accession: JU0274
R;Komase, K.; Haga, T.; Yoshikawa, Y.; Sato, T.A.; Yamanouchi, K.
Virus Genes 4, 173-181, 1990
A;Title: Molecular analysis of structural protein genes of the Yamagata-1 strain of defec
A;Reference number: JU0274; MUID:90385702; PMID:1698327
A;Accession: JU0274
A;Molecule type: mRNA
A;Residues: 1-534 <KOM>
A;Cross-references: EMBL:D10548; NID:g222256; PIDN:BAA01405.1; PID:g222257
A;Note: the authors translated the codon GTA for residue 459 as Gly and GGG for residue 4
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-107/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;108-534/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;498-514/Domain: transmembrane #status predicted <TMN>
F;6,29,61,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 32.5%; Score 79; DB 1; Length 534;
Best Local Similarity 70.8%; Pred. No. 0.026;
Matches 17; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

```
Qy          19 LSEIKGVIVHRLEGV----GGEHW 38
               ||||||||||||||    | : |
Db         288 LSEIKGVIVHRLEGVSYNIGSQEW 311
```

RESULT 7
VGNZRK
cell fusion glycoprotein precursor - rinderpest virus (strain Kabete O)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: A31051
R;Hsu, D.; Yamanaka, M.; Miller, J.; Dale, B.; Grubman, M.; Yilma, T.
Virology 166, 149-153, 1988
A;Title: Cloning of the fusion gene of rinderpest virus: comparative sequence analysis w
A;Reference number: A31051; MUID:88322864; PMID:3413983
A;Accession: A31051
A;Molecule type: genomic RNA

```
A;Residues: 1-546 <HSU>
A;Cross-references: UNIPROT:P12574
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-108/Product: cell fusion glycoprotein F2 #status predicted <FF1>
F;109-546/Product: cell fusion glycoprotein F1 #status predicted <FF2>
F;109-134/Domain: transmembrane #status predicted <TN1>
F;491-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63,518/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             32.5%;  Score 79;  DB 1;  Length 546;
  Best Local Similarity   59.3%;  Pred. No. 0.027;
  Matches   16;  Conservative    3;  Mismatches    4;  Indels    4;  Gaps    1;

Qy         16 FGGLSEIKGVIVHRLEGV----GGEHW 38
              :  ||||||||:||||||    | : |
Db        281 YPSLSEIKGVIIHRLEGVSYNIGSQEW 307


RESULT 8
S47305
gene F protein - rinderpest virus
C;Species: rinderpest virus
C;Date: 20-Oct-1994 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S47305; S47301
R;Baron, M.D.; Barrett, T.
submitted to the EMBL Data Library, March 1994
A;Description: The sequence of the N and L genes of Rinderpest virus, and the 5O and 3O
A;Reference number: S47283
A;Accession: S47305
A;Molecule type: mRNA
A;Residues: 1-546 <BAR>
A;Cross-references: UNIPROT:P41356; EMBL:Z30697; NID:g535396; PIDN:CAA83181.1; PID:g5354
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: transmembrane protein

  Query Match             32.5%;  Score 79;  DB 2;  Length 546;
  Best Local Similarity   59.3%;  Pred. No. 0.027;
  Matches   16;  Conservative    3;  Mismatches    4;  Indels    4;  Gaps    1;

Qy         16 FGGLSEIKGVIVHRLEGV----GGEHW 38
              :  ||||||||:||||||    | : |
Db        281 YPSLSEIKGVIIHRLEGVSYNIGSQEW 307


RESULT 9
E48556
cell fusion glycoprotein precursor - measles virus (strain AIK-C)
C;Species: measles virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: E48556
R;Mori, T.; Sasaki, K.; Hashimoto, H.; Makino, S.
Virus Genes 7, 67-81, 1993
A;Title: Molecular cloning and complete nucleotide sequence of genomic RNA of the AIK-C
A;Reference number: A48556; MUID:93227570; PMID:8470368
A;Accession: E48556
A;Molecule type: genomic RNA
A;Residues: 1-550 <MOR>
A;Cross-references: UNIPROT:P35973; GB:S58435; NID:g299460; PIDN:AAB26145.1; PID:g299465
A;Note: sequence extracted from NCBI backbone (NCBIN:129264, NCBIP:129272)
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-107/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;108-550/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;113-138/Region: hydrophobic
F;495-514/Domain: transmembrane #status predicted <TMM>
F;6,29,61,67/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             32.5%;  Score 79;  DB 1;  Length 550;
  Best Local Similarity   70.8%;  Pred. No. 0.027;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              ||||||||||||||    | : |
Db        288 LSEIKGVIVHRLEGVSYNIGSQEW 311


RESULT 10
VGNZMV
cell fusion glycoprotein precursor - measles virus
C;Species: measles virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A26962; A25616; PQ0380; PQ0384
R;Buckland, R.; Gerald, C.; Barker, R.; Wild, T.F.
J. Gen. Virol. 68, 1695-1703, 1987
A;Title: Fusion glycoprotein of measles virus: nucleotide sequence of the gene and compa
A;Reference number: A92794; MUID:87224816; PMID:3585281
A;Accession: A26962
A;Molecule type: mRNA
A;Residues: 1-553 <BUC>
A;Cross-references: UNIPROT:O93055; GB:D00090; NID:g222061; PIDN:BAA00056.1; PID:g222062
A;Experimental source: strain Halle
R;Richardson, C.; Hull, D.; Greer, P.; Hasel, K.; Berkovich, A.; Englund, G.; Bellini, W
Virology 155, 508-523, 1986
A;Title: The nucleotide sequence of the mRNA encoding the fusion protein of measles viru
A;Reference number: A94350; MUID:87071668; PMID:3788062
A;Accession: A25616
A;Molecule type: mRNA
A;Residues: 4-553 <RIC>
A;Cross-references: GB:M14915; NID:g331762; PIDN:AAA46423.1; PID:g331763
A;Experimental source: strain Edmonston
R;Schulz, T.F.; Hoad, J.G.; Whitby, D.; Tizard, E.J.; Dillon, M.J.; Weiss, R.A.
J. Gen. Virol. 73, 1581-1586, 1992
A;Title: A measles virus isolate from a child with Kawasaki disease: sequence comparison
A;Reference number: PQ0374; MUID:92300360; PMID:1607874
A;Accession: PQ0380
A;Molecule type: genomic RNA
A;Residues: 272-553 <SCH1>
A;Experimental source: isolate CL
A;Accession: PQ0384
A;Molecule type: genomic RNA
A;Residues: 272-553 <SCH2>
A;Experimental source: isolate SE
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-110/Product: cell fusion glycoprotein F2 #status predicted <FF2>
F;111-553/Product: cell fusion glycoprotein F1 #status predicted <FF1>
F;501-517/Domain: transmembrane #status predicted <TMN>
F;32,64,70/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             32.5%;  Score 79;  DB 1;  Length 553;
  Best Local Similarity   70.8%;  Pred. No. 0.027;
  Matches   17;  Conservative    1;  Mismatches    2;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              ||||||||||||||    | : |
Db        291 LSEIKGVIVHRLEGVSYNIGSQEW 314


RESULT 11
RHMSG
gonadoliberin precursor - mouse
N;Alternate names: gonadotropin-releasing hormone (GnRH); luteinizing hormone releasing H
N;Contains: gonadoliberin; gonadoliberin-associated protein (GAP)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 18-Mar-1997 #text_change 09-Jul-2004
C;Accession: A47578
```

R;Mason, A.J.; Hayflick, J.S.; Zoeller, R.T.; Young III, W.S.; Phillips, H.S.; Nikolics,
Science 234, 1366-1371, 1986
A;Title: A deletion truncating the gonadotropin-releasing hormone gene is responsible fo
A;Reference number: A47578; MUID:87069928; PMID:3024317
A;Accession: A47578
A;Molecule type: DNA
A;Residues: 1-90 <MAS>
A;Cross-references: UNIPROT:P13562; EMBL:M14872; NID:g193576; PIDN:AAA37717.1; PID:g3871
C;Genetics:
A;Introns: 45/3; 77/3
C;Function:
A;Description: gonadoliberin stimulates pituitary secretion of lutropin and follitropin
A;Note: gonadoliberin-associated protein may have prolactin release inhibiting activity
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;22-31/Product: gonadoliberin #status predicted <GLB>
F;35-90/Product: gonadoliberin-associated protein #status predicted <GAP>
F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;31/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

  Query Match 30.5%; Score 74; DB 1; Length 90;
  Best Local Similarity 75.0%; Pred. No. 0.016;
  Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 30 LEGVGGEHWSYGLRPG 45
||| :|||||||||
Db 16 LEGCSSQHWSYGLRPG 31

RESULT 12
RHRTG
gonadoliberin precursor - rat
N;Alternate names: gonadoliberin-associated protein (GAP); gonadotropin releasing hormon
N;Contains: gonadoliberin; prolactin release-inhibiting factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A40147; B26173; A48410
R;Bond, C.T.; Hayflick, J.S.; Seeburg, P.H.; Adelman, J.P.
Mol. Endocrinol. 3, 1257-1262, 1989
A;Title: The rat gonadotropin-releasing hormone: SH locus: structure and hypothalamic ex
A;Reference number: A40147; MUID:89384661; PMID:2476669
A;Accession: A40147
A;Molecule type: DNA
A;Residues: 1-92 <BON>
A;Cross-references: UNIPROT:P07490; GB:M31670; NID:g204447; PIDN:AAA41264.1; PID:g204448
R;Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H.
Proc. Natl. Acad. Sci. U.S.A. 83, 179-183, 1986
A;Title: Isolation of the gene and hypothalamic cDNA for the common precursor of gonadot
A;Reference number: A94090; MUID:86094338; PMID:2867548
A;Accession: B26173
A;Molecule type: mRNA
A;Residues: 1-92 <ADE>
A;Cross-references: GB:M12579; NID:g204445; PIDN:AAA41263.1; PID:g204446
R;Maier, C.C.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E.
Cell. Mol. Neurobiol. 12, 447-454, 1992
A;Title: Thymocytes express a mRNA that is identical to hypothalamic luteinizing hormone
A;Reference number: A48410; MUID:93105480; PMID:1468115
A;Accession: A48410
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <MAI>
A;Cross-references: GB:S50870; NID:g262059; PIDN:AAB24572.1; PID:g262060
A;Experimental source: thymus
A;Note: sequence extracted from NCBI backbone (NCBIN:121082, NCBIP:121083)
C;Genetics:
A;Introns: 47/3; 79/3
C;Function:
A;Description: stimulates pituitary secretion of lutropin and follitropin
A;Note: gonadoliberin-associated protein may have prolactin release inhibiting activiy
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid; r
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-92/Product: progonadoliberin #status predicted <PGN>
F;24-33/Product: gonadoliberin #status predicted <GLN>
F;37-92/Product: prolactin release-inhibiting factor #status predicted <PIF>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following glyc

  Query Match 30.5%; Score 74; DB 1; Length 92;
  Best Local Similarity 75.0%; Pred. No. 0.016;
  Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 30 LEGVGGEHWSYGLRPG 45
||| :|||||||||
Db 18 LEGCSSQHWSYGLRPG 33

RESULT 13
VGNZRL
cell fusion glycoprotein precursor - rinderpest virus (strain L)
N;Contains: fusion glycoprotein F1; fusion glycoprotein F2
C;Species: rinderpest virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A28921
R;Tsukiyama, K.; Yoshikawa, Y.; Yamanouchi, K.
Virology 164, 523-530, 1988
A;Title: Fusion glycoprotein (F) of rinderpest virus: entire nucleotide sequence of the
A;Reference number: A28921; MUID:88219541; PMID:3285575
A;Accession: A28921
A;Molecule type: mRNA
A;Residues: 1-546 <TSU>
A;Cross-references: UNIPROT:P10864; GB:M20870; NID:g333898; PIDN:AAA47399.1; PID:g333899
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-104/Product: cell fusion glycoprotein F2 #status predicted <FG2>
F;105-546/Product: cell fusion glycoprotein F1 #status predicted <FG1>
F;109-133/Domain: transmembrane #status predicted <TN1>
F;485-513/Domain: transmembrane #status predicted <TN2>
F;25,57,63/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 30.5%; Score 74; DB 1; Length 546;
  Best Local Similarity 59.3%; Pred. No. 0.12;
  Matches 16; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

Qy 16 FGGLSEIKGVIVHRLEGV----GGEHW 38
: ||||||||||||| | | : |
Db 281 YPSLSEIKGVIVHRLESVSYNIGSQEW 307

RESULT 14
JQ2223
cell fusion protein F0 precursor - phocine distemper virus
N;Contains: F1 and F2 chains
C;Species: phocine distemper virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JQ2223
R;Visser, I.K.G.; van der Heijden, R.W.J.; van de Bildt, M.W.G.; Kenter, M.J.H.; Oervell,
J. Gen. Virol. 74, 1989-1994, 1993
A;Title: Fusion protein gene nucleotide sequence similarities, shared antigenic sites an
e virus entity.
A;Reference number: JQ2223; MUID:93389459; PMID:8376973
A;Accession: JQ2223
A;Molecule type: mRNA
A;Residues: 1-542 <VIS>
A;Cross-references: UNIPROT:Q7LZY1; GB:L07075
A;Note: the authors translated the codon ATC for residue 4 as Leu
C;Comment: This fusion protein F0 is cleaved into F1 and F2 chains.
C;Genetics:
A;Gene: F
C;Superfamily: parainfluenza virus cell fusion protein
C;Keywords: glycoprotein; membrane fusion; transmembrane protein
F;1-15/Domain: signal sequence #status predicted <SIG>

```
F;16-542/Product: fusion protein #status predicted <MAT>
F;16-99/Product: F2 chain #status predicted <F2C>
F;105-542/Product: F1 chain #status predicted <F1C>
F;105-135/Region: hydrophobic
F;486-512/Domain: transmembrane #status predicted <TMM>
F;21,53,59,397/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             29.6%;  Score 72;  DB 2;  Length 542;
  Best Local Similarity   62.5%;  Pred. No. 0.22;
  Matches   15;  Conservative    2;  Mismatches    3;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||:|||||||||| |    | : |
Db        280 LSEVKGVIVHRLEAVSYNIGSQEW 303


RESULT 15
S47034
cell fusion protein precursor - porpoise morbillivirus
N;Alternate names: F protein
C;Species: porpoise morbillivirus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S47034
R;Bolt, G.; Gottschalck, E.; Blixenkkrone-Moeller, M.; Wishaupt, R.G.A.; Welsh, M.J.; Ea
submitted to the EMBL Data Library, July 1994
A;Description: Nucleotide sequence comparisons of the F and M genes of cetacean morbilli
A;Reference number: S47034
A;Accession: S47034
A;Molecule type: mRNA
A;Residues: 1-552' <BOL>
A;Cross-references: UNIPROT:Q66147; EMBL:X80757; NID:g520639; PIDN:CAA56731.1; PID:g5206
A;Experimental source: isolate Ulster 88
A;Note: the source is designated as Cetacean morbillivirus
C;Superfamily: parainfluenza virus cell fusion protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-552/Product: fusion protein #status predicted <MAT>

  Query Match             29.6%;  Score 72;  DB 2;  Length 552;
  Best Local Similarity   62.5%;  Pred. No. 0.22;
  Matches   15;  Conservative    2;  Mismatches    3;  Indels    4;  Gaps    1;

Qy         19 LSEIKGVIVHRLEGV----GGEHW 38
              |||:|||||||||| |    | : |
Db        290 LSEVKGVIVHRLEAVSYNLGSQEW 313


Search completed: February  8, 2005, 17:31:34
Job time : 40 secs
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